

OM protein - protein search, using sw model
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Run on: January 29, 2003, 14:10:27 ; Search time 15 Seconds
 (without alignments)
 32.045 Million cell updates/sec

Title: US-09-403-440a-4
 Perfect score: 20
 Sequence: 1 FXXXW 5

Scoring table: BLOSUM62 10.0 , Gapext 0.5

Searched: 283224 seqs., 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Post-processing: Minimum Match 0%, Maximum Match 100%, Listing first 45 summaries

Database : PIR_7.3,*
 1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	9	2 A24244	adipokinetic hormone
2	17	85.0	53	2 T00172	hypothetical prote
3	17	85.0	53	2 D89989	hypothetical prote
4	17	85.0	63	2 T29202	hypothetical prote
5	17	85.0	65	1 A32613	adipokinetic hormone
6	17	85.0	67	2 T12860	hypothetical prote
7	17	85.0	70	2 A66942	hypothetical prote
8	17	85.0	72	2 S15137	thioredoxin h2 - s
9	17	85.0	77	2 S18581	pufQ protein - Rho
10	17	85.0	77	2 T50756	pufQ protein - impo
11	17	85.0	84	2 E92668	hypothetical prote
12	17	85.0	88	2 B46264	thioredoxin in 2 - sl
13	17	85.0	98	2 F47624	Ig heavy chain V-I
14	17	85.0	99	2 S34447	gene E2 protein -
15	17	85.0	99	2 S34448	gene E2 protein -
16	17	85.0	99	2 S37441	gene E2 protein -
17	17	85.0	99	2 S37442	gene E2 protein -
18	17	85.0	99	2 S37444	hypothetical prote
19	17	85.0	102	2 G71043	Gtp-binding protein
20	17	85.0	102	1 B50956	thioredoxin - rabb
21	17	85.0	104	1 A28086	thioredoxin - valid
22	17	85.0	105	1 JH0508	thioredoxin - rhes
23	17	85.0	105	1 JS0657	thioredoxin - rat
24	17	85.0	105	1 S04352	thioredoxin - mouse
25	17	85.0	105	1 S04107	thioredoxin - chick
26	17	85.0	105	1 A30006	hypothetical prote
27	17	85.0	107	2 T33843	thioredoxin [impor
28	17	85.0	108	2 AH2101	Ig heavy chain V-I
29	17	85.0	112	2 PH0980	

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9	17	85.0	77	2 S18581	pufQ protein - Rho
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14	17	85.0	99	2 S34447	gene E2 protein -
15	17	85.0	99	2 S34448	gene E2 protein -
16	17	85.0	99	2 S37441	gene E2 protein -
17	17	85.0	99	2 S37442	gene E2 protein -
18	17	85.0	99	2 S37444	hypothetical prote
19	17	85.0	102	2 G71043	Gtp-binding protein
20	17	85.0	102	1 B50956	thioredoxin - rabb
21	17	85.0	104	1 A28086	thioredoxin - valid
22	17	85.0	105	1 JH0508	thioredoxin - rhes
23	17	85.0	105	1 JS0657	thioredoxin - rat
24	17	85.0	105	1 S04352	thioredoxin - mouse
25	17	85.0	105	1 S04107	thioredoxin - chick
26	17	85.0	105	1 A30006	hypothetical prote
27	17	85.0	107	2 T33843	thioredoxin [impor
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9	17	85.0	77	2 S18581	pufQ protein - Rho
10	17	85.0	77	2 T50756	pufQ protein - impo
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15	17	85.0	99	2 S34448	gene E2 protein -
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17	17	85.0	99	2 S37442	gene E2 protein -
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7	17	85.0	70	2 A66942	hypothetical prote
8	17	85.0	72	2 S15137	thioredoxin h2 - s
9	17	85.0	77	2 S18581	pufQ protein - Rho
10	17	85.0	77	2 T50756	pufQ protein - impo
11	17	85.0	84	2 E92668	hypothetical prote
12	17	85.0	88	2 B46264	thioredoxin in 2 - sl
13	17	85.0	98	2 F47624	Ig heavy chain V-I
14	17	85.0	99	2 S34447</td	

RESULT 3
D89899 hypothetical protein SAS063 [imported] - *Staphylococcus aureus* (strain N315)
C;Species: *Staphylococcus aureus*
C;Accession: D89899 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, T.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, N.; Hayashi, H.; Hiramatsu, K.
C.; Shiba, T.; Hattori, M.; Ogawara, N.; Hayashi, H.; Hiramatsu, K.
A;Title: whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:2311952; PMID:11418146
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-53 <KUR>
A;Cross-references: GB:BA000018; PID:913701784; PIDN:BA043077.1; GSPDB:GN00149
A;Gene: SAS063
C;Genetics:
C;Species: *Caenorhabditis elegans*
C;Accession: T29202
R;Wilson, J.; Wohlbrenn, P.
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A;Description: The Sequence of *C. elegans* cosmid F28F9.
A;Accession: T29202
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-53 <NEL>
A;Cross-references: EMBL:AF020713; NID:93025478; PID:93025574; PIDN:ACI13069.1
A;Gene: CESP:F28F9.3
A;Map position: 4
A;Introns: 38/1
Query Match 85.0%; Score 17; DB 2; Length 53;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 28 FTIAW 32

RESULT 4
T29202
hypothetical protein F28F9.3 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Accession: T29202
R;Wilson, J.; Wohlbrenn, P.
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A;Description: The Sequence of *C. elegans* cosmid F28F9.
A;Accession: T29202
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-53 <NEL>
A;Cross-references: EMBL:AF020713; NID:93025478; PID:93025574; PIDN:ACI13069.1
A;Gene: CESP:F28F9.3
A;Map position: 4
A;Introns: 38/1
Query Match 85.0%; Score 17; DB 2; Length 53;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 28 FTIAW 32

RESULT 5
A32613 adipokinetic hormone precursor - tobacco hornworm
C;Species: *Manduca sexta* (tobacco hornworm)
C;Accession: A32613 #sequence_revision 21-May-1990 #text_change 18-Jun-1999
R;Bradfield, J.Y.; Keeley, L.L.; Biol. Chem. 264, 12793, 1989
A;Title: Adipokinetic hormone gene sequence from *Manduca sexta*.
A;Reference number: A32613; MUID:89327232; PMID:2753887
A;Accession: A32613
A;Molecule type: DNA
A;Gene: SAS063
C;Genetics:
C;Species: *Staphylococcus aureus* (strain N315)
C;Accession: D89899 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, T.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, N.; Hayashi, H.; Hiramatsu, K.
C.; Shiba, T.; Hattori, M.; Ogawara, N.; Hayashi, H.; Hiramatsu, K.
A;Title: whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:2311952; PMID:11418146
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-53 <KUR>
A;Cross-references: GB:BA000018; PID:913701784; PIDN:BA043077.1; GSPDB:GN00149
A;Gene: SAS063
C;Genetics:
C;Species: *Bacillus subtilis* phage SPBc2
C;Accession: T12860
R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.
A;Description: The complete nucleotide sequence of the *Bacillus subtilis* SPbetaac2 pro
A;Reference number: 217583
A;Accession: T12860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-67 <LAZ>
A;Cross-references: EMBL:AF020713; NID:93025478; PID:93025574; PIDN:ACI13069.1
A;Gene: CESP:F28F9.3
A;Map position: 4
A;Introns: 38/1
Query Match 85.0%; Score 17; DB 2; Length 63;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 30 FATAW 34

RESULT 6
T12860
hypothetical protein yopl - *Bacillus subtilis* phage SPBc2
C;Species: *Bacillus subtilis* phage SPBc2
C;Accession: T12860
R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.
A;Description: The complete nucleotide sequence of the *Bacillus subtilis* SPbetaac2 pro
A;Reference number: 217583
A;Accession: T12860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-67 <LAZ>
A;Cross-references: EMBL:AF020713; NID:93025478; PID:93025574; PIDN:ACI13069.1
A;Gene: CESP:F28F9.3
A;Map position: 4
A;Introns: 38/1
Query Match 85.0%; Score 17; DB 2; Length 63;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 30 FATAW 34

RESULT 7
A86942 hypothetical protein [imported] - *Mycobacterium leprae*
C;Species: *Mycobacterium leprae*

C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C; Accession: A89542
 R; Cole, S.T.; Englemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
 ean, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sc
 A; Title: Massive gene decay in the leprosy bacillus.
 A; Reference number: A86909; MUID:21128732; PMID:11234002
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-70 <STO>
 A; Cross-references: GB:AL450380; NID:913092599; PIDN:CAC29773.1; GSDB:GN00147
 C; Genetics:
 C; Gene: ML0265

Query Match 85.0%; Score 17; DB 2; Length 70;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03; Matches 2; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 FXXXW 5
 Db 14 FRISW 18

RESULT 8

S15137 thioredoxin h2 - spinach (fragments)
 C; Species: Spinacia oleracea (spinach)
 C; Date: 25-Feb-1994 #sequence_revision 26-Jul-1996 #text_change 23-May-1997
 C; Accession: S15137
 R; Marcus, F.; Chamberlain, S.H.; Chu, C.; Masiarz, F.R.; Shin, S.; Yee, B.C.; Buchanan,
 Arch. Biochem. Biophys. 287, 195-198, 1991
 A; Title: Plant thioredoxin h: an animal-like thioredoxin occurring in multiple cell comp
 A; Reference number: S15137; MUID:91308382; PMID:1897989
 A; Accession: S15137
 A; Molecule type: protein
 A; Residues: 1-72 <MAR>
 C; Superfamily: thioredoxin; thioredoxin homology
 C; Keywords: redox-active disulfide

Query Match 85.0%; Score 17; DB 2; Length 72;
 Best Local Similarity 40.0%; Pred. No. 1.6e+03; Matches 2; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

QY 1 FXXXW 5
 Db 6 FTASW 10

RESULT 9

S18581 pufQ protein - Rhodobacter sphaeroides
 C; Species: Rhodobacter sphaeroides
 C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Sep-1998
 C; Accession: S18581; S32854
 R; Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.
 Mol. Microbiol. 5, 2649-2661, 1991
 A; Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg
 A; Reference number: S18580; MUID:92140030; PMID:1779756
 A; Accession: S18581
 A; Molecule type: DNA
 A; Status: preliminary
 A; Residues: 1-77 <HUN>
 A; Cross-references: EMBL:X68795; NID:949170; PID:949175
 C; Genetics:
 C; Gene: pufQ
 C; Superfamily: pufQ protein

Query Match 85.0%; Score 17; DB 2; Length 77;
 Best Local Similarity 40.0%; Pred. No. 1.7e+03; Matches 2; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

QY 1 FXXXW 5
 Db 6 FTASW 10

RESULT 10

T50756 pufQ protein [imported] - Rhodobacter sphaeroides
 C; Species: Rhodobacter sphaeroides
 C; Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
 C; Accession: T50756
 R; Choudhary, M.; Kaplan, S.
 Nucleic Acids Res. 28, 862-867, 2000
 A; Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides
 A; Reference number: T25222; MUID:20115911; PMID:10648776
 A; Accession: T50756
 A; Status: preliminary; translated from GB/EMBL/DDJB
 A; Molecule type: DNA
 A; Residues: 1-77 <CHO>
 A; Cross-references: EMBL:AF195122; PIDN:AAF24300.1
 A; Experimental source: strain 2.4.1
 A; Genetics:
 A; Gene: pufQ
 C; Superfamily: pufQ protein

Query Match 85.0%; Score 17; DB 2; Length 77;
 Best Local Similarity 40.0%; Pred. No. 1.7e+03; Matches 2; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

QY 1 FXXXW 5
 Db 60 FASAW 64

RESULT 11

E69268 hypothetical protein AF0149 - Archaeoglobus fulgidus
 C; Species: Archaeoglobus fulgidus
 C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C; Accession: E69268
 R; Kleink, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Weidman, J.F.; McDonald, L.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A; Reference number: A69250; MUID:98069343; PMID:939475
 A; Accession: E69268
 A; Molecule type: nucleic acid sequence not shown; translation not shown
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Residues: 1-84 <KLE>
 A; Cross-references: GB:AE001096; GB:AE00782; NID:92689419; PIDN:AAB91088.1; PID:9265

Query Match 85.0%; Score 17; DB 2; Length 84;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03; Matches 2; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

QY 1 FXXXW 5
 Db 42 FAAW 46

RESULT 12

B46264 thioredoxin 2 - slime mold (Dictyostelium discoideum) (fragment)
 C; Species: Dictyostelium discoideum
 C; Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 11-Jun-1999
 C; Accession: B46264
 R; Wetterauer, B.; Jacquot, J.-P.; Veron, M.
 J. Biol. Chem. 267, 9895-9904, 1992
 A; Title: Thioredoxins from Dictyostelium discoideum are a developmentally regulated m

A;Reference number: A46264; MUID:92250653; PMID:1577820
 A;Accession: B46264
 A;status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-88 <WET>
 C;Cross-references: GB:M91382; NID:916730; PIDN:AAA3259.1; PID:q167931
 I'; 8 - 88/Domain: thioredoxin homology <THR>
 Query Match 85.0%; Score 17; DB 2; Length 88;
 Best Local Similarity 40.0%; Pred. No. 1.8e-03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Lb 26 FSAAW 30

RESULT 13
 F47624

Ig heavy chain V-I region - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)

C;Accession: F47624 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
 J.; EXP. MED. 171, 1721-1737, 1990
 A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation
 A;Reference number: A47624; MUID:90237760; PMID:2110243
 A;Accession: F47624
 A;Status: Preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-98 <HAI>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 P:15-98/bdomain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 17; DB 2; Length 99;
 Best Local Similarity 40.0%; Pred. No. 2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 46 FSTIW 50

Search completed: January 29, 2003, 14:12:36
 Job time : 16 secs

RESULT 14
 S37447

gene E2 protein - human papillomavirus type 5 (fragment)

C;Species: human papillomavirus type 5

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
 C;Accession: S37447
 R;Deau, A.C.
 Submitted to the EMBL Data Library, August 1993
 A;Reference number: S37440
 A;Accession: S37447
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-99 <DEA>
 A;Cross-references: EMBL:X74651; NID:9404204; PIDN:CAA52715.1; PID:9404205
 C;Superfamily: papillomavirus E2 protein

Query Match 85.0%; Score 17; DB 2; Length 99;
 Best Local Similarity 40.0%; Pred. No. 2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 46 FSTIW 50

RESULT 15
 S37448
 gene E2 protein - human papillomavirus type 5 (fragment)

Title:	US-09-403-440A-4									
Perfect score:	20									
Sequence:	1 FXXXW 5									
Scoring table:	BLOSUM62									
Searched:	gapext 0.5									
Total number of hits satisfying chosen parameters:	112892									
Minimum DB seq length:	0									
Maximum DB Seq length:	2000000000									
Post-processing:	Minimum Match 0%									
Listing First 45 summaries										
Database :	SwissProt_40; *									
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES										
Result No.	Score	Query Match	Length	DB ID	Description	RESULT 1	PRT; STANDARD;	PRT;	38 AA.	ALIGNMENTS
-	-	-	-	-	-	PSAI_PR0MA	PSAI_PR0MA			
1	17	85.0	38	1	PSAI_PR0MA	ID: 087785; AC: P08901; DT: 16-OCT-2001 (Rel. 40, Created) DT: 15-JUN-2002 (Rel. 41, Last annotation update)				
2	17	85.0	65	1	AKH_MANSE	PF16069 prochlorococcus marinus				
3	17	85.0	77	1	PUFO_RHOSH	PUFO_RHOSH rhodobacter sphaeroides				
4	17	85.0	84	1	Y149_ARC01	Y149_ARC01 archaeoglobus fumiferans				
5	17	85.0	88	1	THI2_DICDT	THI2_DICDT dictyosphaeliopsis tertia				
6	17	85.0	93	1	CD06_HUMAN	CD06_HUMAN homo sapiens				
7	17	85.0	104	1	THIO_BOVIN	THIO_BOVIN bos taurus				
8	17	85.0	104	1	THIO_CALIA	THIO_CALIA callithrix jacchus				
9	17	85.0	104	1	THIO_CHICK	THIO_CHICK gallus gallus				
10	17	85.0	104	1	THIO_HUMAN	THIO_HUMAN equus caballus				
11	17	85.0	104	1	THIO_MACMU	THIO_MACMU homosapiens				
12	17	85.0	104	1	THIO_OPHRA	THIO_OPHRA ophiolephagus				
13	17	85.0	104	1	THIO_PIG	THIO_PIG sus scrofa				
14	17	85.0	104	1	THIO_RABIT	THIO_RABBIT Oryctolagus cuniculus				
15	17	85.0	104	1	THIO_RAT	THIO_RAT rattus norvegicus				
16	17	85.0	104	1	THIO_SHEEP	THIO_SHEEP ovis aries				
17	17	85.0	107	1	THIO_TOBBC	THIO_TOBBC				
18	17	85.0	112	1	THIH_CHLRE	THIH_CHLRE				
19	17	85.0	114	1	THIL_ARATH	THIL_ARATH arabidopsis thaliana				
20	17	85.0	115	1	THIL_RABTA	THIL_RABTA				
21	17	85.0	115	1	THII_ARATH	THII_ARATH				
22	17	85.0	116	1	THII_FAGES	THII_FAGES				
23	17	85.0	118	1	THII_TOBBC	THII_TOBBC				
24	17	85.0	118	1	THII_ARATH	THII_ARATH				
25	17	85.0	118	1	THII_WHEAT	THII_WHEAT				
26	17	85.0	119	1	THII_WHEAT	THII_WHEAT				
27	17	85.0	119	1	THII_WHEAT	THII_WHEAT				
28	17	85.0	119	1	THII_WHEAT	THII_WHEAT				
29	17	85.0	122	1	THII_WHEAT	THII_WHEAT				
30	17	85.0	122	1	THII_WHEAT	THII_WHEAT				
31	17	85.0	126	1	THII_WHEAT	THII_WHEAT				
32	17	85.0	126	1	THII_WHEAT	THII_WHEAT				
33	17	85.0	126	1	THII_WHEAT	THII_WHEAT				

CS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm), and
 Heliothis zea (Corn earworm) (Bollworm).
 CC Eukaryota; Metazoa; Arthropoda; Pancrustacea; Hexapoda;
 Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 Ditrysia; Sphingiidae; Sphingidae; Sphinginae; Manduca.
 NCBI_TAXID=7130; 7113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.sexta;
 RX MEDLINE=83272322; PubMed=2753887;
 RA Bradfield J.Y.; Keeley L.L.;
 RT "Adipokinetic hormone gene sequence from *Manduca sexta*.";
 RL J. Biol. Chem. 264:12791-12793(1989).
 RN [2]
 RP SEQUENCE OF 20-28.
 RC SPECIES=M.sexta;
 RX MEDLINE=86077009; PubMed=4074373;
 RA Ziebler R.; Eckart K.; Schwarz H.; Keller R.;
 RT "Amino acid sequence of *Manduca sexta* adipokinetic hormone elucidated by combined fast atom bombardment (FAB)-tandem mass spectrometry.";
 RX Biochem. Biophys. Res. Commun. 133:337-342(1985).
 RN [3]
 RP SEQUENCE OF 20-28.
 RC SPECIES=S.zea;
 RX MEDLINE=86186794; PubMed=3964263;
 RA Jaffre H.; Raina A.K.; Riley C.T.; Fraser B.A.; Holman G.M.;
 Wagner R.M.; Ridway R.L.; Hayes D.K.;
 RT "Isolation and primary structure of a peptide from the corpora cardiaca of *Heliothis zea* with adipokinetic activity.";
 RX Blochem. Biophys. Res. Commun. 135:622-628(1986);
 CC FUNCTION: THIS HORMONE RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / RHTH / RPCH FAMILY.
 CC
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 CC
 CC
 DR EMBL; J04972; AAA22999.1; - .
 DR PIR; A32613; A32613.
 DR PIR; A24244; A24244.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00556; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 65
 FT PEPTIDE 20 28
 FT MOD_RES 20 20
 SQ SEQUENCE 65 AA; 7401 MW; 1812E586F2D7852 CRC64;
 Query Match 85.0%; Score 17; DB 1; Length 65;
 Rest Local Similarity 40.0%; Pred. No. 6.9e+02; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXW 5
 Db 23 FTSSW 27
 RESULT 3
 PURO_RHOSH
 ID PURO_RHOSH STANDARD; PRT; 77 AA.
 AC P16569;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.sexta;
 RX MEDLINE=9214030; PubMed=1779756;
 RA Hunter C.N.; McGlynn P.; Ashby M.K.; Burgess J.G.; Olsen J.D.;
 RT "DNA sequencing and complementation/deletion analysis of the bcha-puf operon region of Rhodobacter sphaeroides: in vivo mapping of the oxygen-regulated puf promoter.";
 RX Mol. Microbiol. 5:2649-2661(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
 RX MEDLINE=94245622; PubMed=818896;
 RA Gong L.; Lee J.K.; Kaplan S.;
 RT "The Q gene of Rhodobacter sphaeroides: its role in puf operon expression and spectral complex assembly.";
 RL J. Bacteriol. 176:2946-2961(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
 RX MEDLINE=20115911; PubMed=10648776;
 RA Choudhury M.; Kaplan S.;
 RT "DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2.4.1.";
 RL Nucleic Acids Res. 28:862-867(2000).
 RN [4]
 RP SEQUENCE OF 1-7 FROM N.A.
 RX MEDLINE=91713996; PubMed=8437569;
 RA McGinn P.; Hunter C.N.;
 RT "Genetic analysis of the bchc and bcha genes of Rhodobacter sphaeroides.";
 RL Mol. Gen. Genet. 236:227-234(1993).
 RN [5]
 RP SEQUENCE OF 44-77 FROM N.A.
 RA Kiley P.J.; Bonhag T.J.; Haveka W.A.; Kaplan S.;
 RT "DNA sequence and in vitro expression of the B875 light-harvesting polypeptides of Rhodobacter sphaeroides.";
 RL J. Bacteriol. 169:742-750(1987).
 CC -!- FUNCTION: REQUIRED FOR BACTERIOCHLOROPHYLL BIOSYNTHESIS. DIRECTLY INVOLVED IN THE ASSEMBLY OF BOTH THE B875 AND B800-850 PIGMENT-PROTEIN COMPLEXES.
 CC -!- SIMILARITY: BELONGS TO THE PUFO FAMILY.
 CC
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 CC
 DR EMBL; AJ1010302; CAB38750.1; - .
 DR EMBL; L2584; AAC15241.1; - .
 DR EMBL; AF195122; AAF24300.1; - .
 DR EMBL; M5105; - ; NOT_ANNOTATED_CDS.
 DR PIR; S18581; S18581.
 KW Photosynthesis; Chlorophyll biosynthesis.
 FT CONFICTR 36 36 A->G ([N REF. 1];
 SQ SEQUENCE 77 AA; 8656 MW; 61127EF70B39EB6 CRC64;
 Query Match 85.0%; Score 17; DB 1; Length 77;
 Best Local Similarity 40.0%; Pred. No. 7.9e+02; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DR PIR; S18581; S18581.
 KW Photosynthesis; Chlorophyll biosynthesis.
 FT CONFICTR 36 36 A->G ([N REF. 1];
 DR EMBL; L2584; AAC15241.1; - .
 DR EMBL; AF195122; AAF24300.1; - .
 DR EMBL; M5105; - ; NOT_ANNOTATED_CDS.
 DR PIR; S18581; S18581.

OX NCBI_TaxID=44689;
 RN [1]—
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9225053; PubMed=1577820;
 RA Wetterauer B.; Jacquot J.-P.; Veron M.;
 RT "thioredoxins from Dictyostelium discoideum are a developmentally
 regulated multigene family";
 RT J. Biol. Chem. 267:9895-9904(1992).
 RL -!
 CC FUNCTION: Participates in various redox reactions through the
 reversible oxidation of its active center dithiol to a disulfide
 and catalyzes dithiol-disulfide exchange reactions.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M91382; AAA3259.1; -.
 DR PIR; BA6264; BA6264.
 DR HSSP; P1059; IERV.
 DR DICTYBB; DD05030; txxB.
 DR InterPro; IPR00063; Thior.
 PRAM; PF00085; thiored.
 DR PROSITE; PS00194; THIOREDOXIN: 1.
 KW Redox-active center; Electroneutral; REDOX-ACTIVE (BY SIMILARITY).
 DT DISULFID 31 34
 FT NON_TER 88 88
 SQ SEQUENCE 88 AA; 1010 MW; CECT3BCEFAKB607C CRC64;
 QY 1 FXXW 5
 Query Match 85.0%; Score 17; DB 1; Length 88;
 Best Local Similarity 40.0%; Pred. No. 8.7e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 CC ID CD06_HUMAN
 CC STANDARD; PRT; 93 AA.
 AC 09940;
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Protein C4orf6 (AC1 protein).
 GN C4orf6 OR AC1
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
 OX NCBI_TaxID=9606;
 RN [1]—
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91169148; PubMed=9016955;
 RA Kito K.; Ito T.; Sakaki Y.;
 RT "Fluorescent differential display analysis of gene expression in
 differentiating neuroblastoma cells.";
 RT Gene 184:73-81(1997).
 CC -!
 CC TISSUE SPECIFICITY: EXPRESSED IN NEUROBLASTOMA.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; D82070; HGNC:13716; C4orf6.
 DR Genew; HGNC:13716; C4orf6.

RESULT 4
 Y149_ARCFU STANDARD; PRT; 84 AA.
 ID Y149_ARCFU
 AC 030088;
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Hypothetical protein AF0149.
 GN AF0149.
 OS Archaeoglobus fulgidus.
 OC Archaeobacteria; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]—
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-15 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9384745;
 RA Klein H.-P.; Tomb J.-F.; White O.; Nelson K.E.;
 RA Ketchum K.A.; Dodson R.J.; Gwyn M.; Hickey E.K.; Peterson J.D.;
 RA Richardson D.L.; Kerlavage A.R.; Graham D.E.; Kyrides N.C.;
 RA Fleischmann R.D.; Quackenbush J.; Lee N.H.; Sutton G.G.; Gill S.;
 RA Kirkness E.F.; Dougherty B.A.; McKenney K.; Adams M.D.; Loftus B.;
 RA Peterson S.; Reich C.I.; McNeil J.H.; Badger J.H.; Glodek A.; Zhou L.;
 RA Overbeek R.; Gocayne J.D.; Weilman J.F.; McDonald L.; Utterback T.;
 RA Cotton M.D.; Spriggs T.; Artiach P.; Kaine B.P.; Sykes S.M.;
 RA Sadow P.W.; D'Andrea K.P.; Bowman C.; Fujii C.; Garland S.A.;
 RA Mason T.M.; Olsen G.J.; Fraser C.M.; Smith H.O.; Woese C.R.;
 RA Venier J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 CC -!
 CC SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AE001096; AA91088.1; -.
 DR TIGR; AF0149; -.
 DR EMBL; AE001096; AA91088.1; -.
 DR TIGR; AF0149; -.
 KW Hypothetical protein; transmembrane; Complete proteome.
 FT TRANSMEM 4 POTENTIAL.
 FT TRANSMEM 20 POTENTIAL.
 FT TRANSMEM 27 POTENTIAL.
 FT TRANSMEM 59 POTENTIAL.
 SQ SEQUENCE 84 AA; 8893 MW; E2FDFF1FC6FBF1EE CRC64;
 OX
 Query Match 85.0%; Score 17; DB 1; Length 84;
 Best Local Similarity 40.0%; Pred. No. 8.4e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OX 1 FXXXW 5
 DB 42 FRAAW 46

RESULT 5
 TH12_DICDI STANDARD; PRT; 88 AA.
 ID TH12_DICDI
 AC P29446;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thioredoxin 2 (Fragment).
 GN TRXB OR TRXZ.
 OS dictyostelium discoideum (Slime mold); Dictyostelium
 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

SQ SEQUENCE 93 AA: 10499 MW: A8786AC4A9990215 CRC64;
 Query Match 85.0%; Score 17; DB 1; Length 93;
 Best Local Similarity 40.0%; Pred. No. 9.1e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 69 FAASW 73

RESULT 7
 THIO_BOVIN STANDARD; PRT; 104 AA.
 ID THIO_BOVIN DE Thioredoxin.
 AC 097680; GN TXN OR TRX.
 DT 16-OCT-2001 (Rel. 40, created)
 (Rel. 40, last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thioredoxin
 GN TXN.

OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC NCBI_TaxID=9913;

RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=2157430; PubMed=11719593;
 RA Lopata A., Sibson M.C., Enders A.C., Bloomfield K.L., Gregory M.S.,
 RA Trapani G.D., Perkins A.V., Tonissen K.F., Clarke F.M.,
 RT "Expression and localization of thioredoxin during early implantation
 in the marmoset monkey";
 RL Mol Hum Reprod. 7:1159-1165(2001).

CC -!- FUNCTION: Participates in various redox reactions through the
 reversible oxidation of its active center dithiol to a disulfide
 and catalyzes dithiol-disulfide exchange reactions.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.

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CC DR EMBL; AF353204; AAK30295. 1; -.
 CC DR HSSP; P10599; IERT.
 CC DR InterPro; IPR00063; Thiored.
 CC DR Pfam; PF00085; thiored; 1.
 CC DR PRINTS; PRO0421; THIOREDOXIN.
 CC DR PROSITE; PS00194; THIOREDOXIN; 1.
 CC DR KW Redox-active center; Electron transport.
 CC FT INIT-MET 0 BY SIMILARITY.
 CC FT DISUFLID 31 BY SIMILARITY.

SQ SEQUENCE 104 AA: 11681 MW: 506CF93696A2208D CRC64;
 Query Match 85.0%; Score 17; DB 1; Length 104;
 Best Local Similarity 40.0%; Pred. No. 9.9e+02; Length 104;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 26 FSATW 30

RESULT 9
 THIO_CHICK STANDARD; PRT; 104 AA.
 ID THIO_CHICK DE Thioredoxin.
 AC P08629; DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thioredoxin
 GN OS Gallus gallus (chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=88257080; PubMed=2838473;
 RA Jones S.W., Luk K.-C.;
 RT "Isolation of a chicken thioredoxin cDNA clone. Thioredoxin mRNA is
 differentially expressed in normal and Rous sarcoma virus-transformed
 chicken fibroblasts";
 RL J. Biol. Chem. 263:9607-9611(1988);
 CC -!- FUNCTION: Participates in various redox reactions through the
 reversible oxidation of its active center dithiol to a disulfide

CC and catalyzes dithiol-disulfide exchange reactions (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.

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CC

DR EMBL; J03982; AAA49092.1; -.

DR PIR; A30006; A30005.

DR HSSP; P10599; LERT.

DR InterPro; IPR000063; Thioredoxin.

DR Pfam; PF00085; thiored; 1.

DR PRINTS; PR00421; THIOREDOXIN.

DR PROSITE; PS00194; THIOREDOXIN; 1.

FT Redox-active center; Electron transport.

FT INIT_MET 0 BY SIMILARITY.

FT DISULFID 31 REDOX-ACTIVE (BY SIMILARITY).

FT INIT_MET 0 Redox-active center; Electron transport.

FT DISULFID 31 Redox-active center; Electron transport.

FT QY 1 FXXXW 5

FT SEQUENCE 104 AA; 11569 MW; 60366B759010BB12 CRC64;

FT Best Local Similarity 40.0%; Pred. No. 9.9e+02;

FT Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 26 FSATW 30

RESULT 10

THIO_HORSE	STANDARD:	PRT:	104 AA.
ID THIO_HORSE			
AC 097508			
DT 15-JUN-2002 (Rel. 41, Created)			
DT 15-JUN-2002 (Rel. 41, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Thioredoxin (ATL-derived factor) (ABP) (Surface associated sulphhydryl protein) (SASP)			
DE TXN OR TRDX OR TRX OR TRXL			
GN Homo sapiens (Human).			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheridia; Primates; Catarhini; Hominidae; Homo.			
OC NCBI-TAXID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=91340156; PubMed=1874447;			
RT "Isolation and characterization of human thioredoxin-encoding genes.";			
RL Gene 102:221-228(1991).			
RP SEQUENCE FROM N.A.			
RX MEDLINE=89000454; PubMed=3170595;			
RA Wollman E.E., D'Auriol L., Rimsky L., Shaw A., Jacquot J.-P., Wingfield P., Gruber P., Desarpais F.;			
RT "Cloning and expression of a cDNA for human thioredoxin.";			
RL J. Biol. Chem. 263:15506-15512(1988).			
RP SEQUENCE FROM N.A.			
RX MEDLINE=89251607; PubMed=2785919;			
RA Tagaya Y., Medea Y., Matsui A., Kudo N., Matsui H., Hamuro J., Brown N., Arai K.-I., Yoko T., Wakasugi H., Yodoi J.			
RT "ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioredoxin: possible involvement of dithiol-reduction in the IL-2 receptor induction";			
RL EMBO J. 8:757-764(1989).			
RP SEQUENCE FROM N.A.			
RC TISSUE=Lens;			
RA Reddy P.G., Bhuyan D.K., Bhuyan K.C.;			
RC Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
RN [5] SEQUENCE FROM N.A.			
RP TISSUE=Lens;			
RA Liu A., Lou M.F.;			
RT "Cloning, purification and characterization of human lens thioredoxin";			
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.			
RN [6] SEQUENCE FROM N.A.			
RC TISSUE=Brain;			
RA Xu J.Y., Xu L., Li K.S., Dai R.;			
RT "Cloning and sequencing of thioredoxin cDNA from human brain.";			
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
RN [7] SEQUENCE FROM N.A.			
RC TISSUE=Cervix;			
RA Straubberg R.;			
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			

[8] RN
REF SEQUENCE OF 1-14; PubMed=198498;
RX MEDLINE=91151337;
RA Martin H.; Dean M.;
RT "Identification of a thioredoxin-related protein associated with
R1 plasma membranes";
R2 Biochem. Biophys. Res. Commun. 175:123-128(1991).
RN [9]
RT STRUCTURE BY NMR.
RX MEDLINE=9057393; PubMed=2684271;
RA Forman-Kay J.D., Clore G.M., Dricoll P.C., Wingfield P.,
RA Richards F.M., Gronenborn A.M.;
R1 "A proton nuclear magnetic resonance assignment and secondary
RT structure determination of recombinant human thioredoxin";
R2 Biochemistry 28:7088-7097(1989).
RN [10]
RP STRUCTURE BY NMR.
RX MEDLINE=91153399; PubMed=2001356;
RA Forman-Kay J.D., Clore G.M., Wingfield P., Gronenborn A.M.;
RT "High-resolution three-dimensional structure of reduced recombinant
R1 human thioredoxin";
R2 Biochemistry 30:2685-2698(1991).
RN [11]
RP STRUCTURE BY NMR.
RX MEDLINE=95006318; PubMed=7922028;
RA Qin J., Clore G.M., Gronenborn A.M.;
RT "The high-resolution three-dimensional solution structures of the
R1 oxidized and reduced states of human thioredoxin";
R2 Structure 2:503-522(1994).
RN [12]
RP STRUCTURE BY NMR.
RX MEDLINE=96347359; PubMed=8736558;
RA Qin J., Clore G.M., Kennedy W.P., Kuszewski J., Gronenborn A.M.;
RT "The solution structure of human thioredoxin complexed with its
target from Ref-1 reveals peptide chain reversal";
R2 Structure 4:613-620(1996).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX MEDLINE=96399719; PubMed=8860557;
RA Weichsel A., Gasdaska J.R., Powis G., Montfort W.R.;
RT "Crystal structures of reduced, oxidized, and mutated human
thioredoxins: evidence for a regulatory homodimer";
R1 Structure 4:735-751(1996).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF MUTANT ASN-60.
RX MEDLINE=98039128; PubMed=9569465;
RA Andersen J.F., Sanders D.A., Gasdaska J.R., Weichsel A., Powis G.,
RA Montfort W.R.;
RT "Human thioredoxin homodimers: regulation by pH, role of aspartate
R1 60, and crystal structure of the aspartate 60 --> asparagine
mutant";
R2 Biochemistry 36:13979-13988(1997).
RN [15]
RP ACTIVITY.
RX MEDLINE=91097576; PubMed=2176490;
RA Jacquot J.-P., de Lamotte F., Pontecav M., Schuermann P.,
RA Decottignies P., Miginac-Maslow M., Wollman E.;
RT "Human thioredoxin reactivity structure/function relationship";
R1 Biochem. Biophys. Res. Commun. 173:1377-1381(1990).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
-!- FUNCTION: ADF AUGMENTS THE EXPRESSION OF THE INTERLEUKIN-2
CC RECEPTOR TAC (IL2R/P55).
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cyttoplasmic.
CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.

[8] CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC -----
RA DR EMBL; X77584; CAA54687.1; --.
RA DR EMBL; X54540; CAA38410.1; JOINED.
RA DR EMBL; X54541; CAA38410.1; JOINED.
RA DR EMBL; AF26919; AAF6466.1; --.
RA DR EMBL; AF04872; AAF87085.1; --.
RA DR EMBL; AF31911; AAG4699.1; --.
RA DR EMBL; BC003377; AAH03377.1; --.
RA DR PIR; A31993; A31993.
RA DR PIR; S04106; S04106.
RA DR PIR; JH0568; JH0568.
RA DR PDB; 3TRX; 15-JAN-93.
RA DR PDB; 4TRX; 15-JAN-93.
RA DR PDB; 1TRS; 30-SEP-94.
RA DR PDB; 1ERV; 14-OCT-96.
RA DR PDB; 1TRW; 14-OCT-95.
RA DR PDB; 1CQG; 01-AUG-96.
RA DR PDB; 1ICQH; 01-AUG-96.
RA DR PDB; 1IMDI; 03-JUN-95.
RA DR PDB; 1MDJ; 20-JUL-95.
RA DR PDB; 1MDK; 20-JUL-95.
RA DR PDB; 1AUC; 25-FEB-98.
RA DR SWISS-2DPAGE; P10599; HUMAN.
RA DR Harris/Ghent-2DPAGE; 8006; IEF.
RA DR PHC1-2DPAGE; P10599; --.
RA DR Sienda-2DPAGE; P10599; --.
RA DR Genew; HGNC:1435; TXN.
RA DR MIM; 187700; --.
RA DR InterPro; IPR00063; thiored.
RA DR Pfam0005; thiored; I.
RA DR PRINS; PR00421; THIOREDOXIN.
RA DR PROSITE; PS00194; THIOREDOXIN; 1.
RA KW Redox-active center; Electron transport; 3D-structure.
FT INIT-MET 0 0
FT DISUFDID 31 34 REDOX-ACTIVE.
FT DISUFDID 72 72 INTERCHAIN.
FT CONFFLICT 38 38 K -> N (IN REF. 2 AND 4).
FT CONFLICT 73 73 M -> T (IN REF. 2 AND 4).
FT STRAND 2 3
FT HELIX 7 16
FT TURN 18 19
FT STRAND 22 27
FT HELIX 32 35
FT TURN 36 37
FT HELIX 38 41
FT TURN 42 43
FT HELIX 44 47
FT STRAND 52 57
FT TURN 58 60
FT HELIX 62 68
FT TURN 69 69
FT STRAND 75 80
FT TURN 81 82
FT STRAND 83 89
FT HELIX 94 103
FT SEQUENCE 104 AA; 11606 MW; 7FFABDF3B6FBE33A CRC64;

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Query Match 85.0%; Score 17; DB 1; Length 104;

Best Local Similarity 40.0%; Pred. No. 9.9e+02;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXX 5

DR EMBL; AK007537; BAB25096_1; -
 DR EMBL; AK007790; BAB25256_1; -
 DR EMBL; BC010756; AAH10756_1; -
 DR PIR; S04107; SV4107.
 DR HSSP; P10599; IERT.
 DR SWISS-2DPAGE; P10639; MOUSE.
 DR MGD; MGII_98874; TxnL.
 DR InterPro; IPR000063; Thioredoxin.
 DR Pfam; PF00085; thiored; 1.
 DR PRINTS; PRO0421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Redox-active center; Electron transport.
 FT INIT-MET 0
 FT DISULFID 31 34 REDOX-ACTIVE (BY SIMILARITY).
 DR PRINTS; PRO0421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Redox-active center; Electron transport.
 FT INIT-MET 0
 FT DISULFID 31 34 REDOX-ACTIVE (BY SIMILARITY).
 SQ SEQUENCE 104 AA; 1154 MW; 60BE619609AC773 CRC64;
 Query Match 85.0%; Score 17; DB 1; Length 104;
 Best Local Similarity 40.0%; Pred. No. 9.9e+02; 0; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 26 FSATW 30

RESULT 14
 THIO_OPHHA STANDARD; PRT; 104 AA.

ID THIO_OPHHA
 AC 09871; 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thioredoxin.
 GN TXN
 OS Ophiophagus hannah (King cobra) (Naja hannah).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Futeleostomi;
 OC Elapidae; Elapinae; Ophiophagidae;
 OX NCBI_TAXID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RA Yu G.W., Xu J.Y., Xu L., Cheung P.Y., Lee K.S.;
 RT "The cloning and expression of porcine thioredoxin in E. coli.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE OF 1-33.
 RC TISSUE-Erythrocyte;
 RA Lee K.S., Tang W.K., Cheung P.Y., Siu Y.L., Wong N.S.;
 RL Submitted (MAY-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: Participates in various redox reactions through the reversible oxidation of its active center dithiol to a disulfide and catalyzes dithiol-disulfide exchange reactions.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (By similarity).
 CC -!- TISSUE SPECIFICITY: ERYTHROCYTE.
 CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF082821; AAK60272_1; -
 DR HSSP; P10599; IERV
 DR InterPro; IPR000063; Thioredoxin.
 DR Pfam; PF00085; thiored; 1.
 DR PRINTS; PRO0421; THIOREDOXIN; 1.
 DR Redox-active center; Electron transport.
 FT INIT-MET 0
 FT DISULFID 31 34 REDOX-ACTIVE (BY SIMILARITY).
 SQ SEQUENCE 104 AA; 11697 MW; 9B16FF9696A2396A CRC64;
 Query Match 85.0%; Score 17; DB 1; Length 104;
 Best Local Similarity 40.0%; Pred. No. 9.9e+02; 0; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 26 FSATW 30

Search completed: January 29, 2003, 14:11:37
 Job time : 11 secs

Query Match 85.0%; Score 17; DB 1; Length 104;

DR HSSP: P46939; IBHD.
 DR InterPro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 FT NON_TER 38 38
 SEQUENCE 38 AA; 4424 MW; 41C67E01642ABCBD0 CRC64;
 Query Match 85.0%; Score 17; DB 13; Length 38;
 Best Local Similarity 40.0%; Pred. No. 2.e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 32 FTSSW 36

RESULT 6
 Q9PV89 PRELIMINARY; PRT; 40 AA.
 ID Q9PV89
 AC 09PV89;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Dystrophin (Fragment).
 GN DYST.
 OS Triakis sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
 NCBI_TaxID:94228;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DYS16SHARK; MEDLINE=99398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Breiner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate
 evolution";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL; AP130783; AAD54177.1; -.
 DR HSSP; P46939; IBHD.
 DR InterPro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 FT NON_TER 1 1
 SEQUENCE 40 AA; 4604 MW;
 Query Match 85.0%; Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 32 FTSSW 36

RESULT 7
 Q9PV88 PRELIMINARY; PRT; 40 AA.
 ID Q9PV88
 AC 09PV88;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Dystrophin (Fragment).
 GN DYST.
 OC Torpedo californica (Pacific electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalea; Hylosqualea; Pristioraja; Batroidea;
 OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
 NCBI_TaxID=7787;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DYSTORP; MEDLINE=99398697; PubMed=10468597;

RESULT 8
 Q9PV85 PRELIMINARY; PRT; 40 AA.
 ID Q9PV85
 AC 09PV85;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Dystrophin (Fragment).
 GN OSTEOGLOSSUM sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 Osteoglossiformes; Osteoglossidae; Osteoglossum.
 NCBI_TaxID:27725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DYSTDRACONFTSH; MEDLINE=99398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "late changes in spliceosomal introns define clades in vertebrate
 evolution";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL; AP13087; AAD54181.1; -.
 DR HSSP; P46939; IBHD.
 DR InterPro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 FT NON_TER 1 1
 SEQUENCE 40 AA; 40 MW;
 Query Match 85.0%; Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 32 FTSSW 36

RESULT 9
 Q9PV84 PRELIMINARY; PRT; 40 AA.
 ID Q9PV84
 AC 09PV84;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Dystrophin (Fragment).
 GN DYST.
 OS Anguilla sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC

CC Anguilla.
 CX NCBI_TaxID=62126;
 RN [1]_SEQUENCE FROM N_A.
 RP STRAIN=DYSTGEEL;
 RX MEDLINE=93398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate
 evolution";
 RL PROC. NATL. ACAD. SCI. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF137088; AA154182.1; -.
 DR HSSP; P46339; 1BHD.
 DR Interpro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 DR PROSITE; PS50021; CH; 1.
 FT NON_TER 1 1
 FT NON_TER 40 40
 SQ SEQUENCE 40 AA; 4574 MW; 557846E66BDB5437 CRC64;
 Db 32 FSSSW 36

RESULT 10
 Q9PV82 PRELIMINARY; PRT; 40 AA.
 ID Q9PV82; OC 01-MAY-2000 (TREMBIrel. 13, Created)
 DT 01-JUN-2002 (TREMBIrel. 21, Last annotation update)
 DE Dystrophin (Fragment).
 RA [1]
 GN Barbus tetrazona.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Barbus.
 DR NCBI_TaxID=94221;

SEQUENCE FROM N_A.
 RC STRAIN=DYSTGEELBARB;
 RX MEDLINE=93398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate
 evolution";
 RL PROC. NATL. ACAD. SCI. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF137090; AA051841.1; -.
 DR HSSP; P46339; 1BHD.
 DR Interpro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 FT NON_TER 1 1
 FT NON_TER 40 40
 SQ SEQUENCE 40 AA; 4573 MW; 459B37C19BC3E736 CRC64;

Query Match Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 Db 32 FSSSW 36

RESULT 11
 Q9PV81 PRELIMINARY; PRT; 40 AA.
 DR Dystrophin (Fragment).
 DE DYSTGEEL;
 RN [1]_SEQUENCE FROM N_A.
 RP STRAIN=DYSTGEEL;
 RX MEDLINE=93398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate
 evolution";
 RL PROC. NATL. ACAD. SCI. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF137092; AA05186.1; -.
 DR HSSP; P4693; 1BHD.
 DR Interpro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 FT NON_TER 1 1
 FT NON_TER 40 40
 SQ SEQUENCE 40 AA; 4512 MN; B4931BF59BD542A CRC64;

Query Match Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 Db 32 FSSSW 36

RESULT 12
 Q9PV80 PRELIMINARY; PRT; 40 AA.
 ID Q9PV80; OC 01-MAY-2000 (TREMBIrel. 13, Created)
 DT 01-MAY-2000 (TREMBIrel. 13, Last sequence update)
 DR 01-JUN-2002 (TREMBIrel. 21, Last annotation update)
 DE Dystrophin (Fragment).
 RA [1]
 GN Plecoglossus altivelis.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
 OC Proctacanthopterygii; Salmoniformes; Osmeridae; Plecoglossus.
 DR NCBI_TaxID=61084;

SEQUENCE FROM N_A.
 RC STRAIN=DYSTGEAU;
 RX MEDLINE=93398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate
 evolution";
 RL PROC. NATL. ACAD. SCI. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF137092; AA05186.1; -.
 DR HSSP; P4693; 1BHD.
 DR Interpro; IPR001715; Calponin-like.
 DR Pfam; PF00307; CH; 1.
 FT NON_TER 1 1
 FT NON_TER 40 40
 SQ SEQUENCE 40 AA; 4512 MN; B4931BF59BD542A CRC64;

Query Match Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 Db 32 FSSSW 36

RESULT 13

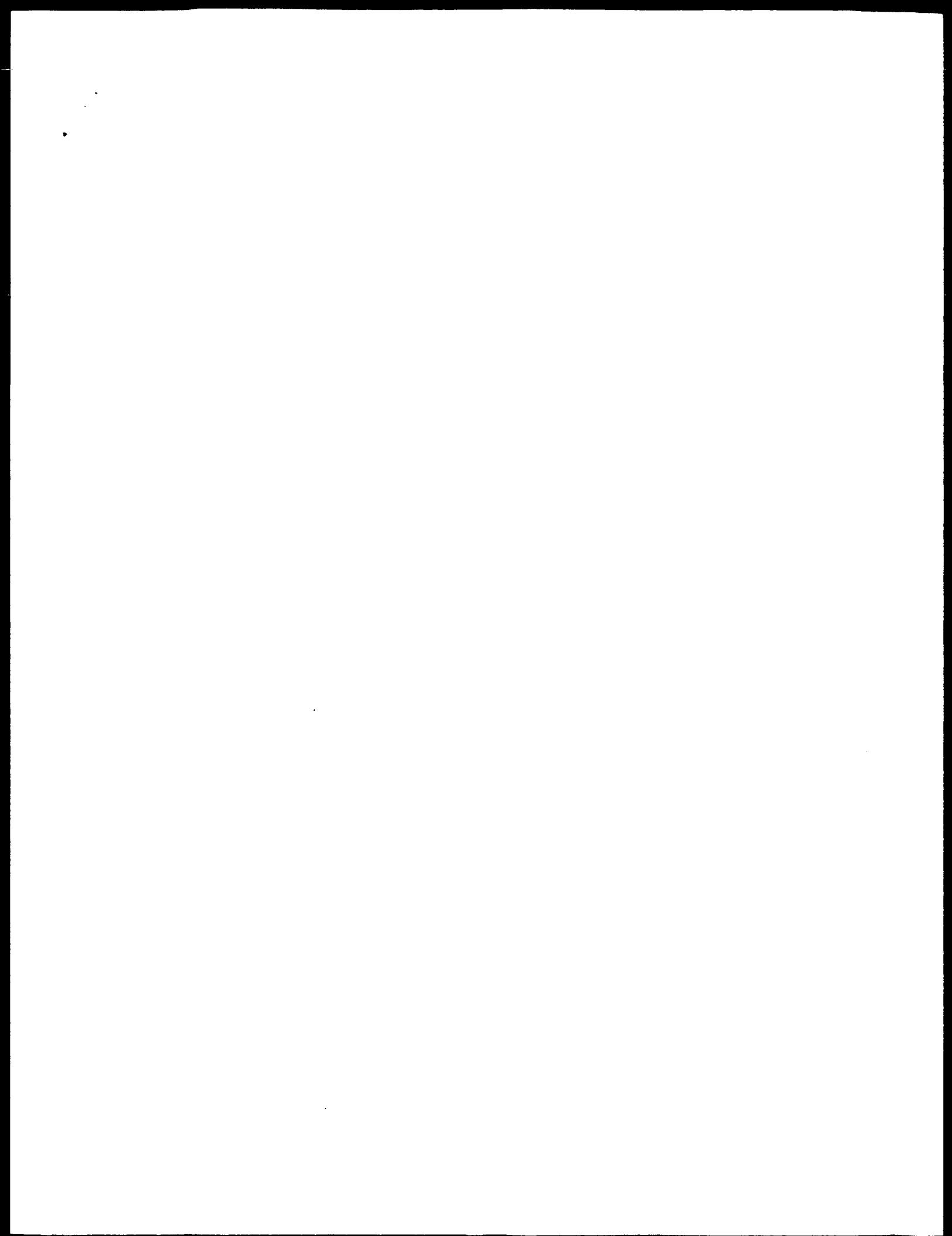
Q9PT24
 ID Q9PT24 PRELIMINARY; PRT; 40 AA.
 AC Q9PT24;
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Dystrophin (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (*Salmo gairdneri*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DYST6TROUT; PubMed=10468597;
 RA MEDLINE=99398697;
 Venkatesh B., Ning Y., Brenner S.;
 "Late changes in spliceosomal introns define clades in vertebrate
 evolution";
 Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 RL EMBL: AF137093; AAD54187.1; .
 DR HSSP: P46939; IBHD.
 DR InterPro: IPR001715; Calponin-like.
 DR Pfam: PF00307; CH; 1.
 RT NON_TER 1 40 40
 SEQUENCE 40 AA; 4551 MW; B4865AA19BDB4B17 CRC64;
 Query Match 85.0%; Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 SQ Qy 1 FXXXW 5
 |
 Db 32 FSSSW 36

RESULT 14
 Q9PV79 PRELIMINARY; PRT; 40 AA.
 AC Q9PV79;
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-JUN-2002 (TREMBrel. 13, Last sequence update)
 DE Dystrophin (Fragment).
 GN
 OS Galaxias maculatus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC protacanthopterygii; Salmoniformes; Galaxiidae; Galaxias.
 NCBI_TaxID=61620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DYST6GAL;
 RX MEDLINE=99398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 "Late changes in spliceosomal introns define clades in vertebrate
 evolution";
 Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 RL EMBL: AF137096; AAD54189.1; .
 DR HSSP: P46939; IBHD.
 DR InterPro: IPR001715; calponin-like.
 DR Pfam: PF00307; CH; 1.
 RT NON_TER 1 40 40
 SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;
 Query Match 85.0%; Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 SQ Qy 1 FXXXW 5
 |
 Db 32 FSSSW 36

Search completed: January 29, 2003, 14:12:13
 Job time : 30 secs

Query Match 85.0%; Score 17; DB 13; Length 40;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5



PT Detecting infection by acid-fast microbes for diagnosis of *Helicobacter pylori*, comprises reacting a faecal sample with two binding reagents for antigens that survive intestinal passage -

PS Claim 26; Page 22; 84pp; German.

CC This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a faecal sample with at least two different monoclonal antibodies (Mab) (or their fragments or derivatives) or aptamers (collectively (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of (Ag). These epitopes are present, after passage through the intestines, in at least some mammals, and have either: (i) their native structure; or (ii) a structure against which an antibody is produced by an animal infected or immunized with (A), or its extract. Lysates, derived by an animal or fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera *Helicobacter*, *Mycobacterium* and *Campylobacter*, specifically *H. pylori*, *H. hepaticus*, *M. tuberculosis*, *C. jejuni* and *C. pylori*. (I) may also be used therapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequence represents a fragment of a *H. pylori* beta-urease-binding antibody heavy chain complementarity determining region CDR1 which is used to illustrate the method of the invention.

SQ Sequence 10 AA;

Query Match 85.0%; Score 17; DB 21; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.5e+03; Gaps 0;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 4 FSTSW 8

RESULT 2

AAB86058
ID AAB86058 standard; Peptide; 10 AA.
XX

AC AAB86058;

XX
DT 17-JUL-2001 (first entry)

DE H. pylori beta-urease derived antibody light chain CDR1 #1.

KW Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen; infection; acid-resistant microorganism; fecal; antibody; diagnosis; antibacterial; complementary determining region.

OS Unidentified.

XX WO200127613-A2.

XX PE 19-APR-2001.

PF 12-OCT-2000; 2000WO-EP10058.

PR 12-OCT-1999; 99EP-012051.

PR 16-MAR-2000; 2000EP-010559.

PR 31-MAR-2000; 2000EP-0107028.

PR 10-MAY-2000; 2000EP-0110110.

PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

XX PI Reiter C, Culmann G, Heppner P, Ringel A, Mueller H, Haindl E;

XX DR WPI; 2001-282087/29.

XX DR N-PSDB; AAF88060.

PT Detecting infections by acid-resistant microorganisms, particularly for diagnosing *Helicobacter pylori*, comprises an immunoassay on a fecal sample -

PS Claim 23; Page 17; 89pp; German.

CC This invention describes a novel method for detecting, in a mammal, infection by an acid-resistant microorganism (A) which comprises reacting a fecal sample with: (i) a receptor (R) such that a complex is formed with an antigen (Ag) of (A); or (ii) two different R so that a three-part complex is formed with Ag, and the formation of a complex detected. R are specific for an Ag which, after passage through the intestines, at least in some mammals, retains a native (or corresponding) structure against which the mammal produces antibodies (when immunized or infected with (A) or its extracts, lysates or derived proteins (or fragments) or synthetic peptides). The products of the invention have antibacterial activity. The method is used to diagnose infection by *Helicobacter*, *Campylobacter* or *Mycobacterium*, particularly *H. pylori* (most preferred), *H. hepatica*, *C. jejuni* and *M. tuberculosis*, and also to monitor the progress of treatment. Receptors, particularly antibodies, directed against Ag can be used therapeutically for treatment of infections. The method requires only one R to provide a reasonably secure diagnosis (although use of two R improves sensitivity), so is relatively inexpensive and more easily standardized. Also it is direct, non-invasive, suitable for automation and may indicate the stage of an infection. This sequence represents a complementarity determining region (CDR) from an antibody generated against a *Helicobacter pylori* antigen (catalase or beta-urease) which is used to illustrate the method of the invention.

XX SQ Sequence 10 AA;

Query Match 85.0%; Score 17; DB 22; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.5e+03; Gaps 0;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 4 FSTSW 8

RESULT 3

AAB86090
ID AAB86090 standard; Peptide; 10 AA.
XX
AC AAB86090;
XX
DT 17-JUL-2001 (first entry)

DE H. pylori beta-urease derived antibody light chain CDR1 #1.

KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope; acid-resistant microorganism; complementary determining region; CDR; feces; heavy chain; light chain.

OS Unidentified.

XX WO200127612-A2.

XX PD 19-APR-2001.

PF 12-OCT-2000; 2000WO-EP10057.

PR 12-OCT-1999; 99EP-0120351.

PR 16-MAR-2000; 2000EP-0105592.

PR 31-MAR-2000; 2000EP-0107028.

PR 10-MAY-2000; 2000EP-0110110.

PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

XX PI Reiter C, Culmann G, Lakner M, Truee A, Dehnert S, Schwartz G;

XX DR WPI; 2001-282086/29.

XX	DR	N-PSB; AAF88117.
PT	Detecing infections by acid-resistant microorganisms, particularly for	
PT	detecting Helicobacter pylori, comprises immunochromatographic	
PT	detection of antigen in feces -	
XX	Claim 27; Page 27; 90pp; German.	
PS	This invention describes a novel method for detecting infection by an	
XX	acid-resistant microorganism (A) in a mammal, using	
CC	inexpensive and non-invasive, and may indicate the stage of infection.	
CC	A test strip used in the method may include a filter to eliminate	
CC	particles present in the sample and only a single receptor provides a	
CC	reasonably secure diagnosis, with specificity and selectivity improved	
CC	by detecting several epitopes (of catalase) or different antigens	
CC	(catalase and beta'-urease). The method can be automated. This sequence	
CC	represents a complementarity determining region (CDR) from an antibody	
CC	raised against the H. pylori catalase or beta'-urease antigen which is	
CC	used to illustrate the method of the invention.	
XX	SQ Sequence 10 AA:	
Query Match 85.0%; Score 17; DB 22; Length 10;		
Best Local Similarity 40.0%; Pred. No. 1.5e+03;		
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
Db 4 FSTSW 8		
Qy 1 FXXXW 5		
Db 4 FSTSW 8		
RESULT 4		
AABG5735 standard; peptide; 13 AA.		
ID AABG5735		
KW AAE05735; standard; peptide; 13 AA.		
AC AAE05735;		
XX 24-SEP-2001 (first entry)		
DT 24-JAN-2002 (first entry)		
DE Complementarity-determining region 3 (CDR3) of MoPhabs #7.		
XX CDR3; complementarity-determining region 3; monoclonal phage antibody;		
KW MoPhabs; antigen.		
XX OS Synthetic.		
XX PN US6265150-B1.		
XX PD 24-JUL-2001.		
XX PF 26-MAY-1998; 98US-0085072.		
PR 07-JUN-1995; 95US-0483633.		
PR 18-SEP-1997; 97US-0932892.		
XX PA (BECT) BECTON DICKINSON & CO.		
PA (CRUC-) CRUCELL HOLLAND BV.		
XX PI Terstappen LW, Logtenberg T;		
XX DR WPI; 2001-463929/50.		
PS Example 6; Column 6; 6pp; English.		
XX	The invention relates to a method of obtaining a phage particle which has an antibody fragment directed against an antigen associated with the surface of target cells in a heterogeneous cell population. The method involves incubating a library of phage particles with the target cells to allow binding of the antibody fragment expressed on the surface of the phage particles to the antigen associated with the target cells. The method is useful for obtaining human antibodies against known and novel surface antigens in their native configuration, expressed on phenotypically defined subpopulations of cells. The present sequence is complementarity-determining region 3 (CDR3) of monoclonal phage antibodies (MoPhabs) used in the exemplification of the invention.	
XX	SQ Sequence 13 AA:	
Query Match 85.0%; Score 17; DB 22; Length 13;		
Best Local Similarity 40.0%; Pred. No. 1.8e+03;		
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
Db 6 FASSW 10		
Qy 1 FXXXW 5		
Db 6 FASSW 10		
RESULT 5		
AAM98088		
ID AAM98088 standard; Peptide; 14 AA.		
XX		
AC AAM98088;		
XX DT 24-JAN-2002 (first entry)		
XX DE Human peptide #1363 encoded by a SNP oligonucleotide.		
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;		
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;		
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;		
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;		
KW complement related protein; cytochrome; kinase; cytokine; integrerin;		
KW interleukin; G-protein coupled receptor; thiosterase; inflammation;		
KW multifactorial disease; autoimmune disease; infection;		
KW nervous system disease.		
XX OS Homo sapiens.		
XX PN WO200147944-A2.		
XX PD 05-JUL-2001.		
XX PF 28-DEC-2000; 2000WO-US35498.		
XX PR 28-DEC-1999; 99US-0173419.		
PR 27-DEC-2000; 2000US-0173419.		
XX PA (CURA-) CURAGEN CORP.		
XX PF Shimkets RA, Leach M;		
XX DR WPI; 2001-46510/50.		
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -		
PS Disclosure; Page 3967; 4143pp; English.		
XX	The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinins, cytokines, interferons interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide.	

the oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Graves' disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney), leukaemia, diseases of the nervous system and an infection of pathogenic organisms.

Sequence 14 AA;

Query Match

85.0%

Score

17

DB

22

Length

14

Best Local Similarity 40.0%; Pred. No. 2.e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 6 FASTW 10

RESULT 6

AAR97874

ID

AAR97874 standard; peptide: 15 AA.

XX

AC

AAR97874;

XX

DT

16-AUG-1996 (first entry)

XX

DE

Japan cedar pollen mature allergen Cry j II amino acids 21-35.

XX

KW

Allergen; epitope; overlapping peptide; cry j II; cedar pollen;

XX

OS

Cryptomeria japonica.

XX

PN

JP08047792-A.

XX

PD

20-FEB-1996.

XX

PR

07-NOV-1994;

XX

PR

26-MAY-1994;

XX

PR

05-NOV-1993;

XX

PA

(MEIPI) MEIJI MILK PROD CO LTD.

XX

DR

WPT; 1996-166249/17.

XX

PT

Japan cedar pollen allergen Cry j II epitope - comprises at least part of specified 460 amino acid protein

XX

PS

Claim 8; Fig 3; 17pp; Japanese.

XX

CC

AAR97871-R97960 are overlapping peptides used for the epitope mapping of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic peptides of it are useful in the diagnosis, prevention and treatment of Sugi pollinosis, the allergic reaction to Japan cedar pollen.

XX

CC

Significant regions of the allergen were identified using the overlapping peptides of the full epitope derived from a Cry j II antigen-specific T cell line. Amino acids 66-80 (AAR97874) and 186-200 (R978608) of the full mature 460 amino acid allergen are the most allergenic of the 90 peptides tested.

XX

SQ

Sequence 15 AA;

XX

PT

Japan cedar pollen allergen Cry j II epitope - comprises at least part of specified 460 amino acid protein

XX

PS

Claim 8; Fig 3; 17pp; Japanese.

XX

CC

AAR97871-R97960 are overlapping peptides used for the epitope mapping of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic peptides of it are useful in the diagnosis, prevention and treatment of Sugi pollinosis, the allergic reaction to Japan cedar pollen.

XX

CC

Significant regions of the allergen were identified using the overlapping peptides of the full epitope derived from a Cry j II antigen-specific T cell line. Amino acids 66-80 (AAR97874) and 186-200 (R978608) of the full mature 460 amino acid allergen are the most allergenic of the 90 peptides tested.

XX

SQ

Sequence 15 AA;

XX

PT

Query Match

85.0%

Score

17

DB

17

Length

15

CC

PD 22-MAY-1998.
 XX
 PT 12-NOV-1997; 97WO-JP04129.
 PR XX
 PR 13-NOV-1996; 96JP-0302053.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 PT Dairiki K, Kino K, Kume A, Sone T;
 XX
 DR WPI; 1998-297617/26.

Peptides derived from Japanese cedar pollen antigens are immunotherapeutic agents - useful for allergy treatment and typing HLA class II molecules in allergy sufferers

Claim 12; Page 29; 50pp; Japanese.

This sequence represents residues 16-30 of the CRY β 2 protein, and is a peptide of the invention. The peptides are derived from Japanese cedar pollen antigens, and are used as immunotherapeutic agents in the treatment of allergy. The peptides can be used for identification and typing of the particular HLA class II molecules in an allergy sufferer, and also for peptide immunotherapy of an allergy. Using these peptides the immunotherapy can be targeted more specifically to the requirements of the individual patient, allowing more effective treatment of an allergy, including those patients for whom treatment with a conventional immunotherapeutic agent is ineffective.

XX Sequence 15 AA;

Query Match	85.0%	Score	17;	DB	19;	Length	15;
Best Local Similarity	40.0%	Pred. No.	2.1e-03;				
Matches	2;	Mismatches	0;	Indels	0;	Gaps	0;

OY 1 FXXW 5
 Db 9 FSTAW 13

RESULT 9

AAE23038	standard; peptide; 19 AA.
----------	---------------------------

AC XX
 AC AAE23038:
 DT 21-AUG-2002 (first entry)

XX Human thioredoxin, 47916 peptide.

XX Human; thioredoxin; 22108; 47916; haemopoietic disorder; leukaemia; cancer; lung; breast; head; neck; prostate; genitourinary tract; cardiovascular disease; angina pectoris; arteriosclerosis; heart failure; brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma; cytostatic; carcinoma; cardiotant; neuroprotective; antiinflammatory; gene therapy; nootropic.

XX Homo sapiens.

PN WO200226803-A2.

PD 04-APR-2002.
 XX
 PF 25-SEP-2001; 2001WO-US29967.

PR XX
 PR 25-SEP-2000; 2000US-235049P.

PA (MILL-) MILLENTUM PHARM INC.

PT Bandaru R, Kapeller-Libermann R;
 XX
 DR WPI; 2002-416475/44.

XX Sequence 19 AA;

Query Match	85.0%	Score	17;	DB	23;	Length	19;
Best Local Similarity	40.0%	Pred. No.	2.5e-03;				
Matches	2;	Mismatches	0;	Indels	0;	Gaps	0;

OY 1 FXXW 5
 Db 4 FSTAW 8

RESULT 10

AAW42165	standard; peptide; 20 AA.
----------	---------------------------

AC XX
 AC AAW42165:
 DT 16 JUN-1998 (first entry)

XX T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.

XX Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2; diagnosis; allergy; spring tree pollen disease; pollinosis.

OS Chamaesyces obtusa.

PN WO9747568-A1.

PD 18-DEC-1997.

PF 12-JUN-1997; 97WO-JP02031.

PR 14-JUN-1996; 96JP-0153527.

PA (MEIP) MEIJI MILK PROD CO LTD.

PT Dairiki K, Kino K;

DR WPI; 1998-052242/05.

XX T-cell epitope peptide portion of Japanese cypress pollen antigens PT Chao1 and Chao2 - used for diagnosis and treatment of spring tree pollen disease

XX PS Claim 2; Page 36; 71PP; Japanese.

XX The present sequence represents a T-cell epitope peptide from Japanese cypress pollen antigen Chao2. The present invention describes peptides which correspond to the T-cell epitope sites on Japanese cypress pollen antigens chao1 and chao2. The peptides can be used as a reagent for the diagnosis of allergy to Japanese cypress pollen, and as an antigen in

XX
 AC
 AAM31077;
 XX
 DT
 17-OCT-2001 (first entry)
 XX
 DE Peptide #5114 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 XX
 genetic disorder.
 XX
 OS Homo sapiens.
 XX
 WO200157272-A2.
 PN
 XX
 PD 15-NOV-2001.
 XX
 PR 30-JAN-2001; 2001WO-US00665.
 XX
 PR 04-FEB-2000; 2000US-180312P.
 PR 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-060841B.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PT Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2002-114183/15.
 XX
 PA Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 PS Claim 27; SEQ ID No 30187; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 1287 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridise at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labelled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemangiomyomatosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Kartagener syndrome, fibrocytic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 Note: The sequence data for this patient did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 27 AA;
 Query Match 85.0%; Score 17; DB 23; Length 27;

Best Local Similarity 40.0%; Pred. No. 3.3e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Search completed: January 29, 2003, 14:11:20
Job time : 36 secs

RESULT 15
AAB09301
ID AAB09301 standard; Protein; 29 AA.
XX
AC AAB09301;
XX
DT 30-AUG-2000 (first entry)
XX Hepatitis GB virus protein sequence SEQ ID NO:428.
XX Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic;
KW infection; detection; characterisation; hepatitis.
OS Hepatitis GB virus.
XX
PN US6051374-A.
XX
PA 18-APR-2000.
XX
PF 07-JUN-1995; 95US-0488445.
XX
PR 14-FEB-1994; 94US-0196030.
PR 13-MAY-1994; 94US-0242654.
PR 29-JUL-1994; 94US-0283314.
PR 23-NOV-1994; 94US-0344185.
PR 30-JAN-1995; 95US-0377557.

PA (ABB0) ABBOTT LAB.
XX
PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
DR WPI: 2000-338307/29.

XX Detecting target hepatitis GB virus nucleic acid in a test sample suspected of containing HGBV comprises reacting the test sample the HGBV polynucleotide probe and detecting the complex that contains target HGBV -

XX
PS Example 18; Column 491-492; 369pp; English.

CC The present invention describe a method for detecting target hepatitis GB virus (HGBV) nucleic acid (THN). In a test sample (T) suspected of containing HGBV. The method involves reacting (T) with a HGBV polynucleotide probe (I) containing 15 contiguous nucleotides, and which selectively hybridises to the HGBV genome or its full complement, and detecting the complex that contains THN, indicating the presence of target HGBV. The method is used for detecting target HGBV nucleic acid in the test sample suspected of containing HGBV and for characterisation of newly ascertained etiological agent of non-A, non-B, non-C, non-D and non-E hepatitis causing agents collectively termed as hepatitis GB virus. AAsA5270 to AAsA549 and AAs0895 to AAs0940 represent nucleotide CC and protein sequences used in the exemplification of the present invention.

XX
SQ Sequence 29 AA;

Query Match 85.0%; Score 17; DR 21; Length 29;
Best local Similarity 40.0%; pred. No. 3.5e+03;
Mismatches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY '1 FXXXW 5
DB 12 FASAW 16

OM protein - protein search, using sw model

Run on: January 29, 2003, 14:12:18 ; Search time 11 Seconds
 (without alignments)
 9.172 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXW 5

Scoring table: BLOSIM62

Gapop 10.0 , Gapext 0.5

Searched: 12226 seqs, 2017851 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%, Listing first 45 summaries

Database : Published Applications, AA:*

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3: /cgn2_6/ptodata/1/pupba/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pupba/US07_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pupba/US07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pupba/US08_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pupba/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pupba/US09_NEW_PUB.pep:*
9: /cgn2_6/ptodata/1/pupba/US10_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pupba/US10_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pupba/US10_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pupba/US60_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pupba/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pupba/US60_PUBCOMB.pep:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	17	85.0	27	10 US-09-864-761-46828 Sequence 46828, A
2	17	85.0	29	8 US-08-424-550-B428 Sequence 428, App
3	17	85.0	40	10 US-09-057-951-6 Sequence 6, Appl
4	17	85.0	40	10 US-09-864-761-46093 Sequence 46093, A
5	17	85.0	40	12 US-10-150-150-6 Sequence 6, Appl
6	17	85.0	44	10 US-09-864-761-35268 Sequence 35268, A
7	17	85.0	46	10 US-09-864-761-35084 Sequence 35084, A
8	17	85.0	71	10 US-09-864-761-45867 Sequence 45867, A
9	17	85.0	75	10 US-09-867-550-510 Sequence 510, App
10	17	85.0	77	12 US-10-001-843-186 Sequence 186, App
11	17	85.0	78	10 US-09-864-761-33877 Sequence 33877, A
12	17	85.0	104	9 US-10-032-482-1 Sequence 1, Appl
13	17	85.0	111	10 US-09-925-980 Sequence 980, App
14	17	85.0	114	10 US-09-891-898-6 Sequence 6, Appl
15	17	85.0	114	10 US-09-993-524-9 Sequence 9, Appl
16	17	85.0	114	10 US-09-992-524-10 Sequence 10, Appl
17	17	85.0	114	10 US-09-992-524-11 Sequence 11, Appl
18	17	85.0	125	10 US-09-925-300-1114 Sequence 114, App
19	17	85.0	134	9 US-10-079-623-564 Sequence 364, APP

ALIGNMENTS

RESULT 1

US-09-864-761-46828

Patent No. US2002048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

APPLICANT: Neomica-X-1

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CURRENT APPLICATION NUMBER: US 60/180,312

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-05-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Anamax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 46828
 LENGTH: 27
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC007739.1
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.66
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61
 US-09-64-761-46828

Query Match 85.0%; Score 17; DB 10; Length 27;
 Best Local Similarity 40.0%; Pred. No. 6e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 4 FSAAW 8

RESULT 2
 US-08-424-550B-428
 Sequence 428, Application US/08424550B
 Patent No. US200201947A1

GENERAL INFORMATION
 APPLICANT: JOHN N. SIMONS
 APPLICANT: TAMI J. PILOT-MATIAS
 APPLICANT: GEORGE J. DAWSON
 APPLICANT: GEORGE G. SCHLAUDER
 APPLICANT: SURESH M. DESAI
 APPLICANT: THOMAS P. LEARY
 APPLICANT: ANTHONY SCOTT MUERHOFF
 APPLICANT: JAMES C. ERKER
 APPLICANT: SHERI L. BUIJK
 APPLICANT: ISA K. MUSHAHWAR
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500

COMPUTER READABLE FORM:
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 COMPUTER TYPE: Diskette
 OPERATING SYSTEM: Windows95
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/057,951
 FILING DATE: 09-APR-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Melkie John, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 09404/046001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein

US-09-057-951-6

Query Match 85.0%; Score 17; DB 10; Length 40;
 Best Local Similarity 40.0%; Pred. No. 7.4e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 6 FSAAW 10

RESULT 4
 US-09-864-761-46093
 Sequence 46093, Application US/09864761
 Patent No. US2002048763A1

GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.

ATTORNEY/AGENT INFORMATION:
 NAME: POREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-3365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 428:

APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aeonica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-03-26
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006660
 PRIOR FILING DATE: 2001-01-30
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 46093
 LENGTH: 40
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AF233390.1
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
 US-09-864-761-46093

RESULT 6
 US-09-864-761-35268
 ; Sequence 35268, Application US/09864761.
 ; Patent No. US20020048769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aeonica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/006667
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/105,150
 FILING DATE: 25-Mar-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/057,951
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 09404/046001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 MOLECULE TYPE: Protein
 TYPE: amino acid
 TOPOLOGY: linear
 LENGTH: 40 amino acids
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-105-150-6

Query Match 85.0%; Score 17; DB 12; Length 40;
 Best Local Similarity 40.0%; Pred. No. 7.4e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 |
 Db 6 FSAW 10

Query Match 85.0%; Score 17; DB 10; Length 40;
 Best Local Similarity 40.0%; Pred. No. 7.4e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 |
 Db 6 FSAW 10

Query Match 85.0%; Score 17; DB 10; Length 40;
 Best Local Similarity 40.0%; Pred. No. 7.4e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 |
 Db 23 FTSSW 27

RESULT 5
 US-10-105-150-6
 Sequence 6, Application US/10105150
 Patent No. US20020119524A1
 GENERAL INFORMATION:
 APPLICANT: Holtzman, Douglas
 TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED PROTEIN FAMILY AND USES THEREOF

PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03 ;
 PRIOR APPLICATION NUMBER: GB 242633,6
 PRIOR FILING DATE: 2000-10-04 ;
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27 ;
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: PCT/US01/006670
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21 ;
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30 ;
 PRIOR APPLICATION NUMBER: US 09/774,203
 NUMBER OF SEQ ID NOS: 4917
 SOFTWARE: Amnonax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 45867
 LENGTH: 71

TYPE: PRN
 ORGANISM: Homo sapiens

FEATURE:
 OTHER INFORMATION: MAP TO ALL1827_9
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.51
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.51
 OTHER INFORMATION: SWISSPROT HIT: Q6262, EVALUE 4.40e-01
 OTHER INFORMATION: EST_HUMAN HIT: AW151498_1, EVALUE 1.00e+00
 US-09-864-761-45867

Query Match 85.0%; Score 17; DB 10; Length 71;
 Best Local Similarity 40.0%; Pred. No. 1.1e+03; Mismatches 0;
 Matches 2; Conservative 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 4 FASSW 8

RESULT 9
 US-09-867-550-510
 ; Sequence 510, Application US/09867550
 ; Patent No. US20020082206A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leach, Martin D.
 ; APPLICANT: Mehraban, Foad,
 ; APPLICANT: Conley, Pamela
 ; APPLICANT: Law, Debbie
 ; APPLICANT: Topper, James
 ; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and

Query Match 85.0%; Score 17; DB 12; Length 77;
 Best Local Similarity 40.0%; Pred. No. 1.1e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 63 FSASW 67

RESULT 11
 US-09-864-761-33877
 ; Sequence 33877, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Acomica X-1
 ; CURRENT APPLICATION NUMBER: US/09/864-761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIORITY APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIORITY APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIORITY APPLICATION NUMBER: US 09/632,366

Query Match 85.0%; Score 17; DB 10; Length 75;
 Best Local Similarity 40.0%; Pred. No. 1.1e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 64 FSSSW 68

RESULT 10
 US-10-001-843-186
 ; Sequence 186, Application US/10001843
 ; Patent No. US20020132255A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Salcedo, Susana
 ; APPLICANT: Macina, Roberto
 ; APPLICANT: Recipon, Herve
 ; APPLICANT: Cafferkey, Robert
 ; APPLICANT: Sun, Yongming
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Turner, Leah
 ; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
 ; FILE REFERENCE: DEX-0267
 ; CURRENT APPLICATION NUMBER: US/10/001,843
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIORITY APPLICATION NUMBER: 60/249,992
 ; PRIOR FILING DATE: 2000-11-20
 ; NUMBER OF SEQ ID NOS: 218
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 186
 ; LENGTH: 77

TYPE: PRN
 ORGANISM: Homo sapien

US-10-001-843-186

Query Match 85.0%; Score 17; DB 12; Length 77;
 Best Local Similarity 40.0%; Pred. No. 1.1e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 63 FSASW 67

PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 2 4263 6
; PRIOR FILING DATE: 2000-10-04
; CURRENT APPLICATION NUMBER: US/10/032,482
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-01-29
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33877
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-032,482-1
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; TITLE OF INVENTION: IMMUNITY
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/10/032,482
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US/09/445,602
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 980
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-300-980
; Query Match 85.0%; Score 17; DB 10; Length 111;
; Best Local Similarity 40.0%; Pred. No. 1.4e+03; 0; Mismatches 3; Indels 0; Gaps 0;
; Matches 2; Conservative 0;
; QY 1 FXXXW 5
; Db 39 FSSSW 43
; RESULT 12
; US-10-032,482-1
; Sequence 1, Application US/10032482
; Publication No. US20020197270A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irvin
; APPLICANT: Roter, Yarad
; APPLICANT: Wolkowicz, Roland
; APPLICANT: Ruiz, Pedro
; APPLICANT: Erez-Aloni, Neta
; APPLICANT: Herkel, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
; APPLICANT: Moloney, Maurice M.

Search completed: January 29, 2003, 14:16:05
Job time : 12 secs

APPLICANT: DALMIA, BIPIN K.
TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
FILE REFERENCE: 034547/0104
CURRENT APPLICATION NUMBER: US/09/897, 898

PRIOR APPLICATION NUMBER: 09/577, 147
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 09/448, 600
PRIOR FILING DATE: 1999-11-24
PRIOR APPLICATION NUMBER: 09/084, 777
PRIOR FILING DATE: 1998-05-27
PRIOR APPLICATION NUMBER: 60/047, 753
PRIOR FILING DATE: 1997-05-27
PRIOR APPLICATION NUMBER: 60/047, 779
PRIOR FILING DATE: 1997-05-28
PRIOR APPLICATION NUMBER: 60/075, 863
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/075, 864
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6
LENGTH: 114
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-897-898-6

RESULT 15
US-09-992-524-9

Query Match 85.0%; Score 17; DB 10; Length 114;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXXW 5
Db 35 FTASW 39

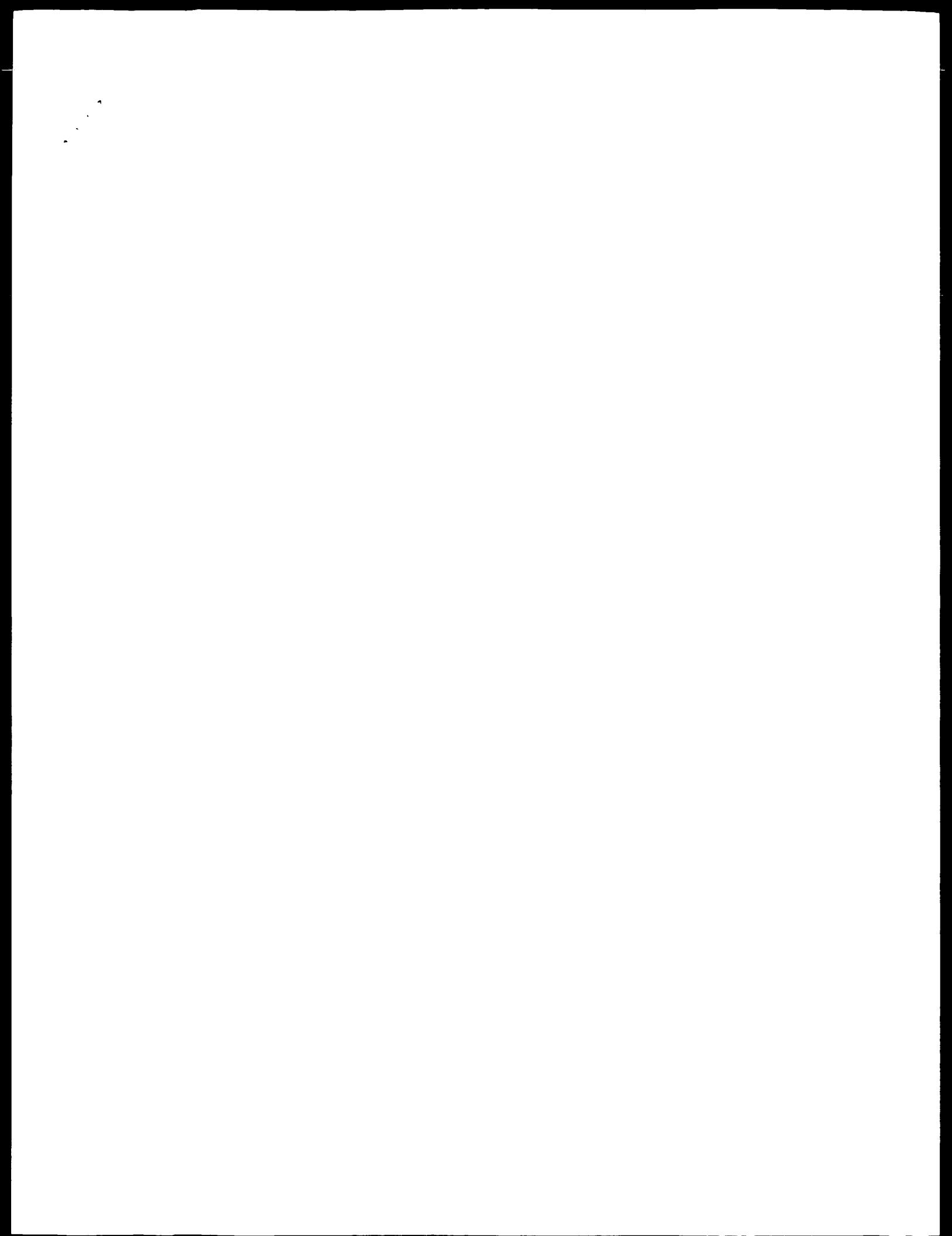
RESULT 15

US-09-992-524-9

; Sequence 9, Application US/09992524
; Patent No. US20020091240A1
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Queen, Cary L.
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
; FILE REFERENCE: 011823-000110S
; CURRENT APPLICATION NUMBER: US/09/992, 524
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/450, 520
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:humanized
; OTHER INFORMATION: immunoglobulin huXAF
US-09-992-524-9

Query Match 85.0%; Score 17; DB 10; Length 114;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 29 FTSSW 33



OM protein - protein search, using sw model

Run on: January 29, 2003, 14:11:27 ; Search time 138 Seconds

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Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 4569144 seqs, 64473310 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- :/cgn2_6/podata/1/paa/us101_COMBO_pep:*
- :/cgn2_6/podata/1/paa/us102_COMBO_pep:*
- :/cgn2_6/podata/1/paa/us60_COMBO_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	17	85.0	9	24 US-10-072-419-3
2	17	85.0	9	24 US-10-072-419-8
3	17	85.0	10	22 US-09-842-776-28
4	17	85.0	10	24 US-10-089-452-36
5	17	85.0	10	25 US-10-110-410-36
6	17	85.0	11	24 US-10-072-419-37

ALIGNMENTS

RESULT 1

US-10-072-419-3

; Sequence 3, Application US/10072419

; GENERAL INFORMATION:

; APPLICANT: Schacter, Bernice

; ATTORNEY: Schacter, Lee

; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in HUMAN CELLS

; FILE REFERENCE: 1073-1

; CURRENT APPLICATION NUMBER: US/10-072,419

; CURRENT FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Apis mellifera

Query Match Score 17; DB 24; Length 9;

Best Local Similarity 85.0%; Pred. No. 4.2e+06; Mismatches 3; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5

Db 4 FTSSW 8

US-10-072-419-3

```

; Sequence 8, Application US/10072419
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human Cells
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-072-419-8

Query Match 85.0%; Score 17; DB 24; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 4 FTSW 8

RESULT 3
US-09-842-776A-28
; Sequence 28, Application US/09842776A
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842-776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIORITY: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 28
; LENGTH: 10
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR) of an antibody heavy chain directed to a beta-urease epitope (alternative sequence)
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease epitope (alternative sequence)
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease epitope (alternative sequence)

Query Match 85.0%; Score 17; DB 24; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 4 FTSW 8

RESULT 4
US-10-089-452-36
; Sequence 36, Application US/10089452
; GENERAL INFORMATION:
; APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
; TITLE OF INVENTION: Improved Method for Detecting Acid Resistant Microorganisms in the Stool
; FILE REFERENCE: D 2394 PCT
; CURRENT APPLICATION NUMBER: US/10/089,452
; CURRENT FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 36
; LENGTH: 10
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: CDR

Query Match 85.0%; Score 17; DB 24; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.6e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 4 FTSW 8

RESULT 5
US-10-110-410-36
; Sequence 36, Application US/10110410
; GENERAL INFORMATION:
; APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
; TITLE OF INVENTION: Immunochromatographic Rapid Test for Detecting Acid Resistant Microorganisms in the Stool
; FILE REFERENCE: D 1805 PCT
; CURRENT APPLICATION NUMBER: US/10/110,410
; CURRENT FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 36
; LENGTH: 10
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: CDR

Query Match 85.0%; Score 17; DB 25; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.6e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 4 FTSW 8

RESULT 6
US-10-072-419-37
; Sequence 37, Application US/10072419
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human Cells
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 37
; LENGTH: 11
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Vanessa cardui
; OTHER INFORMATION: US-10-072-419-37

Query Match 85.0%; Score 17; DB 24; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.7e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 4 FTSW 8

RESULT 7
US-09-355-397C-36

```

GENERAL INFORMATION:
; APPLICANT: SPYCHI, Giannis
; TITLE OF INVENTION: Mammalian Thioredoxin
; FILE REFERENCE: 102041-100
; CURRENT APPLICATION NUMBER: US/09/355, 397C
; CURRENT FILING DATE: 1999-10-18
; PRIORITY APPLICATION NUMBER: PCT/GB98/00263
; PRIORITY FILING DATE: 1998-01-28
; PRIORITY APPLICATION NUMBER: GB 9701710.7
; PRIORITY FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: mammal
; US-09-355-397C-36

Query Match 85.0%; Score 17; DB 17; Length 14;
Best Local Similarity 40.0%; Pred. No. 2e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 5 FSATW 9

RESULT 8
US-09-308-027-12
; Sequence 12, Application US/09308027
GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Kosuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308, 027
; CURRENT FILING DATE: 1999-08-16
; PRIORITY APPLICATION NUMBER: PCT/JP97/04129
; PRIORITY FILING DATE: 1997-11-12
; PRIORITY APPLICATION NUMBER: JP 8/302053
; PRIORITY FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027-12

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 5 FSATW 9

RESULT 9
US-09-308-027-88
; Sequence 88, Application US/09308027
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Kosuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308, 027A
; CURRENT FILING DATE: 1999-08-16
; PRIORITY APPLICATION NUMBER: PCT/JP97/04129
; PRIORITY FILING DATE: 1997-11-12
; PRIORITY APPLICATION NUMBER: JP 8/302053
; PRIORITY FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 88
; LENGTH: 15

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 5 FSATW 9

RESULT 10
US-09-308-027A-12
; Sequence 12, Application US/09308027A
GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Kosuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308, 027A
; CURRENT FILING DATE: 1999-08-16
; PRIORITY APPLICATION NUMBER: PCT/JP97/04129
; PRIORITY FILING DATE: 1997-11-12
; PRIORITY APPLICATION NUMBER: JP 8/302053
; PRIORITY FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027A-12

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 5 FSATW 9

RESULT 11
US-09-308-027A-88
; Sequence 88, Application US/09308027A
GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Kosuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308, 027A
; CURRENT FILING DATE: 1999-08-16
; PRIORITY APPLICATION NUMBER: PCT/JP97/04129
; PRIORITY FILING DATE: 1997-11-12
; PRIORITY APPLICATION NUMBER: JP 8/302053
; PRIORITY FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 88
; LENGTH: 15

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; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027A-88

Query Match      85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04; 0; Mismatches
Matches 2; Conservative 0; Indels 0; Gaps 0;

Qy  1 FXXXW 5
Db  4 FSATW 8

RESULT 12
US-09-963-339-10
; Sequence 10, Application US/09963339
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajashkar
; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
; FILE REFERENCE: 10448-090001
; CURRENT APPLICATION NUMBER: US/09/953, 339
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/235, 049
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-963-339-10

RESULT 13
US-10-145-586-59
; Sequence 59, Application US/10145586
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silos Santiago, Inmaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Weich, Nadine
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS, HUMAN LIGAND-RICH
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN RINGFINGER FAMILY MEMBER
; CURRENT REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145, 586
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 59
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-145-586-59

Query Match      85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04; 0; Mismatches
Matches 2; Conservative 0; Indels 0; Gaps 0;

Qy  1 FXXXW 5
Db  4 FSATW 8

RESULT 14
US-09-202-464-45
; Sequence 45, Application US/09202464
; GENERAL INFORMATION:
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: T-CELL, EPITROPE PEPTIDES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/202, 464
; FILING DATE: 14-Dec-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO JPP97/02031
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: JP 8/153527
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06501-024001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
; US-09-202-464-45

Query Match      85.0%; Score 17; DB 16; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.5e+04; 0; Mismatches
Matches 2; Conservative 0; Indels 0; Gaps 0;

Qy  1 FXXXW 5
Db  8 FTTTW 12

RESULT 15
US-09-240-203B-265
; Sequence 265, Application US/09240203B
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.; Pollock, Joanne; Bond, Julian F.; Garnier, Richard D.; Kuo, Mei-Chang; Powers, Steven P.; Exley, Mark A.; Chen, Xian; Shao, Ze'ev
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; NUMBER OF SEQUENCES: 265
; US-10-145-586-59

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahti & Cockfield, LLP
STREET: 28 State St
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/240,203B

FILING DATE: 22-Jun-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/350,225

FILING DATE: December 6, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandraouras, Esq.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

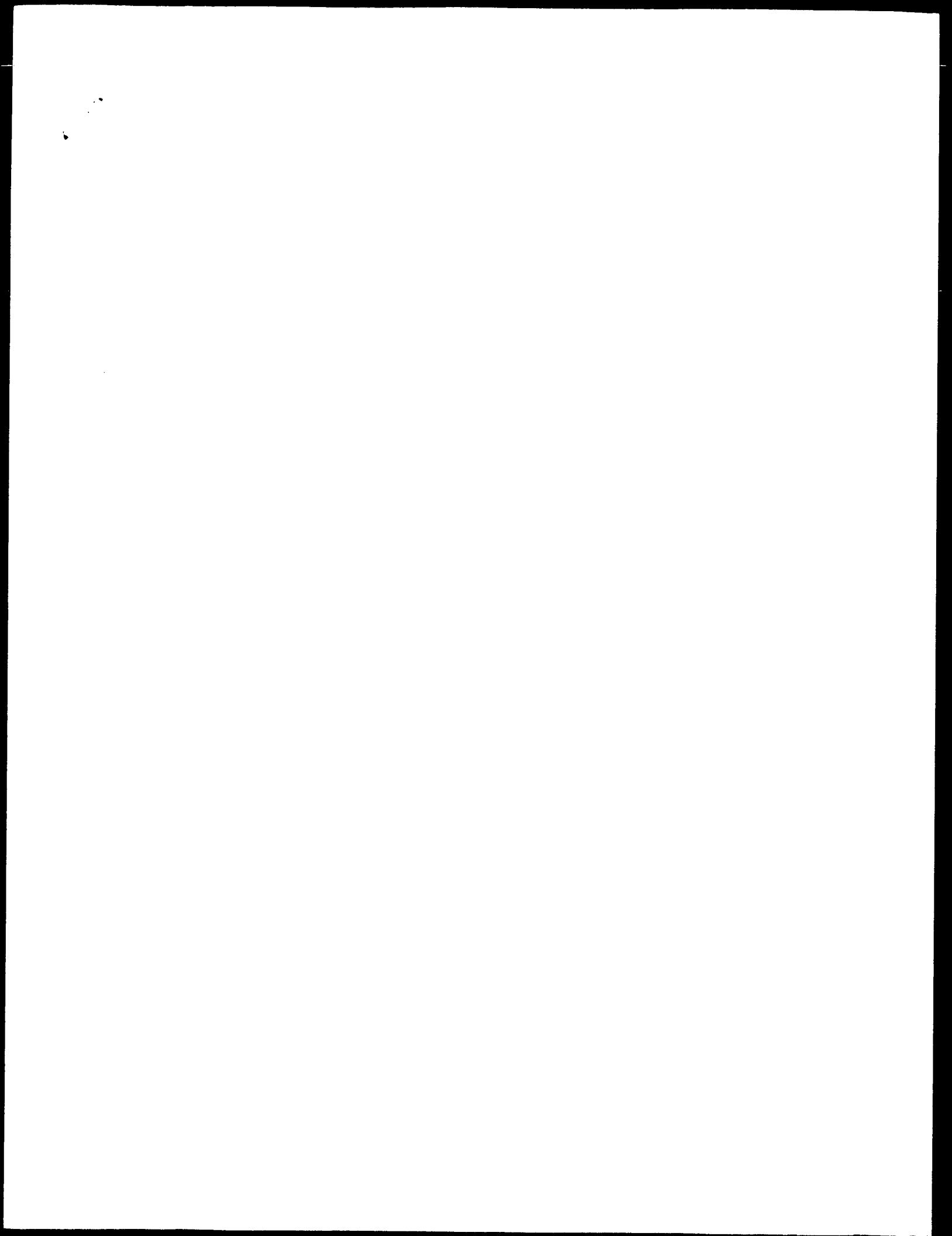
FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-240-203B-265

Query Match 85.0%; Score 17; DB 16; Length: 20;
Best Local Similarity 40.0%; Pred. No. 2.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 FXXW 5
|
Db 12 FSTAW 16

Search completed: January 29, 2003, 14:15:23
Job time : 139 secs



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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:11:42 ; search time 18 Seconds
(without alignments)
21.950 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 396018 seqs, 79020188 residues

Total number of hits satisfying chosen parameters: 396018

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/podata/2/paa/US06_NEW_COMBO.pep.*
3: /cgn2_6/podata/2/paa/US07_NEW_COMBO.pep.*
4: /cgn2_6/podata/2/paa/US08_NEW_COMBO.pep.*
5: /cgn2_6/podata/2/paa/US09_NEW_COMBO.pep.*
6: /cgn2_6/podata/2/paa/US10_NEW_COMBO.pep.*
7: /cgn2_6/podata/2/paa/US60_NEW_COMBO.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	17	85.0	41	5 US-09-966-264D-41
2	17	85.0	44	6 US-10-03-118A-11357
3	17	85.0	46	6 US-10-03-138A-12178
4	17	85.0	51	1 PCT-US03-32727-1679
5	17	85.0	51	1 PCT-US03-32727-19679
6	17	85.0	52	1 PCT-US03-32727-17963
7	17	85.0	52	6 US-10-057-498-17963
8	17	85.0	54	5 US-09-733-648B-21
9	17	85.0	56	1 PCT-US03-32727-29901
10	17	85.0	56	6 US-10-057-498-25901
11	17	85.0	58	1 PCT-US02-32727-8139
12	17	85.0	58	6 US-10-057-498-8139
13	17	85.0	60	1 PCT-US03-32727-6135
14	17	85.0	60	6 US-10-057-498-26135
15	17	85.0	61	1 PCT-US02-32727-7101
16	17	85.0	61	6 US-10-092-41A-4258
17	17	85.0	61	6 US-10-057-498-7101
18	17	85.0	63	1 PCT-US02-32727-3486
19	17	85.0	63	1 PCT-US02-32727-3486
20	17	85.0	67	1 PCT-US02-32727-3015
21	17	85.0	67	6 US-10-057-498-3015
22	17	85.0	68	1 PCT-US02-32727-4894
23	17	85.0	68	6 US-10-057-498-4894
24	17	85.0	69	1 PCT-US02-32727-13373
25	17	85.0	69	1 PCT-US02-32727-13373
26	17	85.0	71	1 PCT-US02-32727-8519

ALIGNMENTS

RESULT 1
US-09-966-264D-41
; Sequence 41, Application US/09966264D
; GENERAL INFORMATION:
; APPLICANT: Barber, Elizabeth K
; TITLE OF INVENTION: Gen Expression Control Element DNA
; FILE REFERENCE: 89603465001
; CURRENT APPLICATION NUMBER: US09/966,264D
; CURRENT FILING DATE: 2001-09-28
; PRIORITY APPLICATION NUMBER: US 60/237,079
; PRIORITY FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 41
; TYPE: PRT
; ORGANISM: human
; US-09-966-264D-41

Query Match 85.0%; Score 17; DB 5'; Length 41;
Best Local Similarity 40.0%; pred. No. 1.8e+03; 0; Mismatches 3; Indels 0; Gaps 0;

QY	1 FXXXW 5	Db	2 FASSW 6

RESULT 2
US-10-203-138A-12357
; Sequence 12357, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenshang
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN BT 474
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIORITY APPLICATION NUMBER: US 60/180,312
; PRIORITY FILING DATE: 04 February 2000 (04-02-00)
; PRIORITY APPLICATION NUMBER: US 60/207,456
; PRIORITY FILING DATE: 26 May 2000 (26-05-00)
; PRIORITY APPLICATION NUMBER: US 09/632,366
; PRIORITY FILING DATE: 03 August 2000 (03-08-00)
; PRIORITY APPLICATION NUMBER: GB 24263.6

RESULT 6
PCT-US02-32727-17963
; Sequence 17963, Application PC/PUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhattacharjee, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Carter, Barrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 17963
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Propioni acnes
; PCT-US02-32727-17963

Query Match 85.0%; Score 17; DB 1; Length 52;
Best Local Similarity 40.0%; Pred. No. 2.1e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; MisMatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 8 FSSSW 12

RESULT 7
US-10-057-498-17963
; Sequence 17963, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhattacharjee, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Barrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10-057-498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29312
; SEQ ID NO 17963
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Propioni acnes
; US-10-057-498-17963

Query Match 85.0%; Score 17; DB 1; Length 52;
Best Local Similarity 40.0%; Pred. No. 2.1e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; MisMatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 8 FSSSW 12

RESULT 8
US-09-733-643B-21
; Sequence 21, Application US/09733643B
; GENERAL INFORMATION:

RESULT 9
PCT-US02-32727-25901
; Sequence 25901, Application PC/PUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhattacharjee, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Barrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 25901
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Propioni acnes
; PCT-US02-32727-25901

Query Match 85.0%; Score 17; DB 1; Length 56;
Best Local Similarity 40.0%; Pred. No. 2.2e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; MisMatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 45 F1STW 49

RESULT 10
US-10-057-498-25901
; Sequence 25901, Application US/10057498

; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes v
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US10/057,498
; CURRENT FILING DATE: 2001-04-20
; SEQ ID NO: 29212
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Propioni acnes
; US-10-057-498-25901

Query Match 85.0%; Score 17; DB 6; Length 56;
Best Local Similarity 40.0%; Pred. No. 2.2e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; MisMatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 45 FTSTW 49

RESULT 11
PCT-US02/32727-8139
Sequence 8139, Application PC/TUS0232727
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatria, Ajay
APPLICANT: Maisonneuve, Jean Francois
APPLICANT: Wang, Sijing
APPLICANT: Jen, Shyan
APPLICANT: Benson, Darin
APPLICANT: Jones, Robert
APPLICANT: Carter, Barrick
APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
APPLICANT: Lodes, Shyian
APPLICANT: Benson, Darin
APPLICANT: Jones, Robert
APPLICANT: Carter, Barrick
APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes v
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO: 26135
LENGTH: 58
TYPE: PRT
ORGANISM: Propioni acnes
PCT-US02/32727-8139

Query Match 85.0%; Score 17; DB 1; Length 58;
Best Local Similarity 40.0%; Pred. No. 2.2e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; MisMatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 45 FTSTW 49

RESULT 12
US-10-057-498-8139
Sequence 8139, Application US/10057498
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes v
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO: 26135
LENGTH: 60
TYPE: PRT
ORGANISM: Propioni acnes
US-10-057-498-26135

Query Match 85.0%; Score 17; DB 6; Length 60;

QY 1 FXXXW 5
Db 34 FTSTW 38

RESULT 13
PCT-US02/32727-26135
Sequence 26135, Application PC/TUS0232727
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatria, Ajay
APPLICANT: Maisonneuve, Jean Francois
APPLICANT: Zhang, Yanni
APPLICANT: Wang, Sijing
APPLICANT: Jen, Shyan
APPLICANT: Benson, Darin
APPLICANT: Jones, Robert
APPLICANT: Carter, Barrick
APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO: 26135
LENGTH: 60
TYPE: PRT
ORGANISM: Propioni acnes
PCT-US02/32727-26135

Query Match 85.0%; Score 17; DB 1; Length 60;
Best Local Similarity 40.0%; Pred. No. 2.3e+03; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 34 FTSTW 38

RESULT 14
US-10-057-498-26135
Sequence 26135, Application US/10057498
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO: 26135
LENGTH: 60
TYPE: PRT
ORGANISM: Propioni acnes
US-10-057-498-26135

Query Match 85.0%; Score 17; DB 6; Length 60;

Best Local Similarity 40.0%; Pred. No. 2.3e+03; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

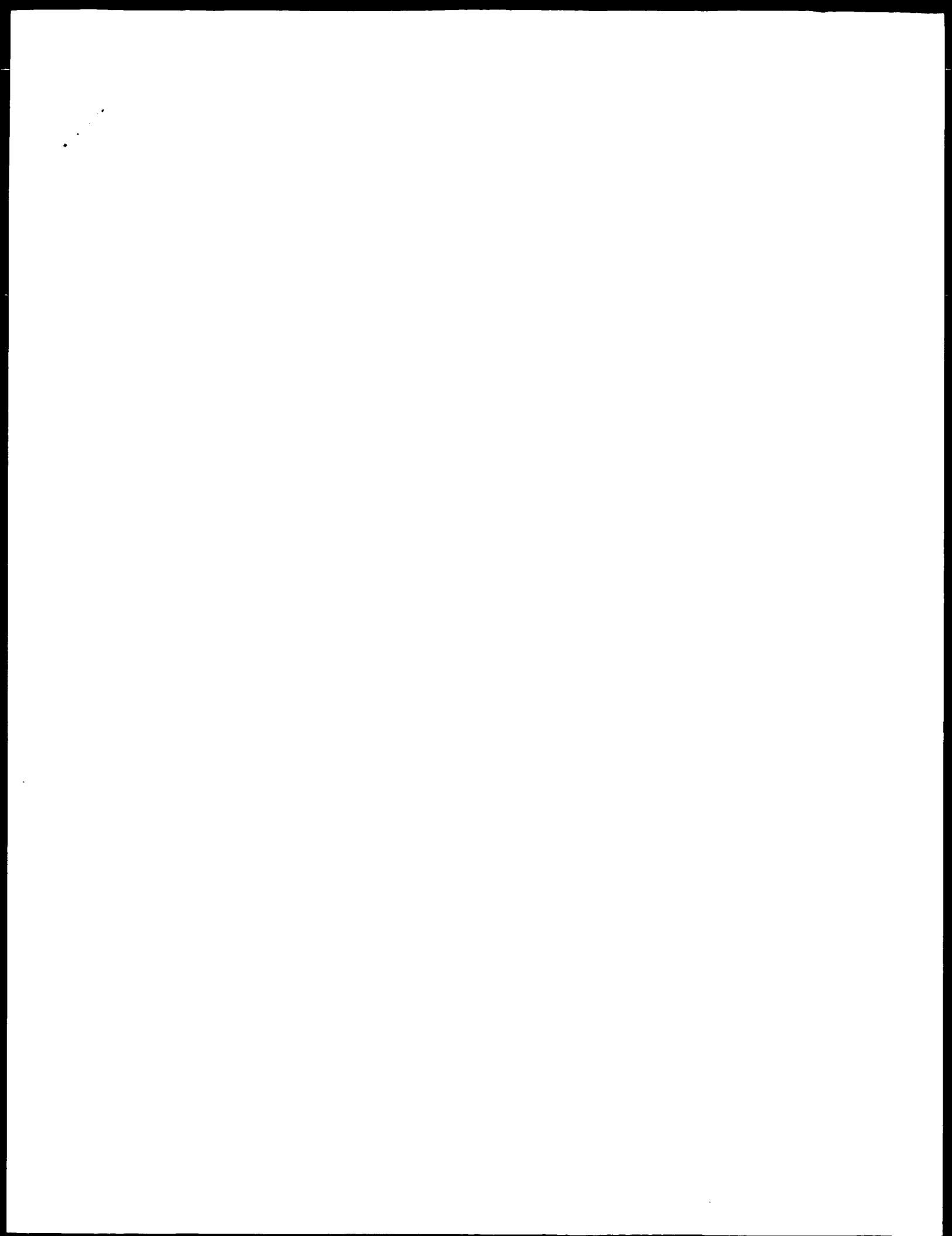
Qy 1 FXXXW 5
 |
 Db 34 FSTTW 38

RESULT 15
 PCT-US02-32727-7101
 ; Sequence 7101, Application PC/US0232727
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Persing, David
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Maisonneuve, Jean Francois
 ; APPLICANT: Zhang, Yanni
 ; APPLICANT: Wang, Siquing
 ; APPLICANT: Jen, Shyian
 ; APPLICANT: Lodes, Michael
 ; APPLICANT: Benson, Darin
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Barth, Brenda
 ; APPLICANT: Douglass, John
 ; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
 ; FILE REFERENCE: 210121.54C1
 ; CURRENT APPLICATION NUMBER: PCT/US02/32727
 ; CURRENT FILING DATE: 2002-10-11
 ; NUMBER OF SEQ ID NOS: 30992
 ; SEQ ID NO 7101
 ; LENGTH: 61
 ;
 ; TYPE: PRT
 ; ORGANISM: Propioni acnes
 PCT-US02-32727-7101

Query Match 85.0%; Score 17; DB 1; Length 61;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 |
 Db 22 FSSSW 26

Search completed: January 29, 2003, 14:15:47
 Job time : 18 secs



OM protein - protein search, using sw model

Run on: January 29, 2003, 14:10:42 ; Search time 15 Seconds

Scoring table: BLOSUM62

Gapext 0.5

Searched: 262574 seqs., 2942222 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/prodata/1/aa/5A_COMBO_pep:*

2: /cgn2_6/prodata/1/aa/5B_COMBO_pep:*

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4: /cgn2_6/prodata/1/aa/6B_COMBO_pep:*

5: /cgn2_6/prodata/1/aa/PCTUS_COMBO_pep:*

6: /cgn2_6/prodata/1/aa/Pbackfilesl_pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	17	85.0	13	4 US-09-085-072-7 Sequence 7, Appli
2	17	85.0	29	4 US-08-419-2604-428 Sequence 428, App
3	17	85.0	34	1 US-08-118-270-134 Sequence 134, App
4	17	85.0	34	1 US-08-118-270-172 Sequence 172, App
5	17	85.0	34	5 PCT-US91-0858-134 Sequence 134, App
6	17	85.0	34	5 PCT-US93-08528-172 Sequence 172, App
7	17	85.0	36	3 US-08-467-023-137 Sequence 137, App
8	17	85.0	37	4 US-09-310-914-10 Sequence 10, Appli
9	17	85.0	41	3 US-08-467-023-136 Sequence 136, App
10	17	85.0	45	3 US-08-467-023-135 Sequence 135, App
11	17	85.0	45	4 US-09-142-476-475 Sequence 475, App
12	17	85.0	49	1 US-08-118-270-209 Sequence 209, App
13	17	85.0	49	5 PCT-US93-08528-209 Sequence 209, App
14	17	85.0	61	4 US-09-134-001C-4258 Sequence 4258, App
15	17	85.0	80	4 US-09-330-914-4 Sequence 4, Appli
16	17	85.0	84	2 US-08-353-476-78 Sequence 78, Appli
17	17	85.0	84	4 US-08-679-493A-97 Sequence 97, Appli
18	17	85.0	91	4 US-08-605-430-19 Sequence 19, Appli
19	17	85.0	91	4 US-08-984-295-3 Sequence 3, Appli
20	17	85.0	102	3 US-08-984-295-3 Sequence 12, Appli
21	17	85.0	102	3 US-08-741-411-12 Sequence 4, Appli
22	17	85.0	104	6 5210073-1 Sequence 78, Appli
23	17	85.0	105	2 US-08-826-910-3 Sequence 3, Appli
24	17	85.0	105	2 US-08-826-910-3 Sequence 4, Appli
25	17	85.0	114	4 US-09-450-520A-9 Sequence 9, Appli
26	17	85.0	114	4 US-09-450-520A-10 Sequence 10, Appli
27	17	85.0	114	4 US-09-450-520A-11 Sequence 11, Appli

ALIGNMENTS

RESULT 1

US-09-085-072-7

; Sequence 7, Application US/09085072

; Patent No. 6265150

; GENERAL INFORMATION:

; APPLICANT: L. Terstappen et al.

; TITLE OF INVENTION: PHAGE ANTIBODIES

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hoffmann & Baron, LLP

; STREET: 350 Jericho Turnpike

; CITY: Jericho

; STATE: New York

; COUNTRY: USA

; ZIP: 11753

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

QUERY APPLICATION NUMBER: US/09/085, 072

FILED DATE: 26-MAY-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Feit, Irving N.

REGISTRATION NUMBER: 28,601

REFERENCE/DOCKET NUMBER: 890-2 FWC/CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 822-3550

TELEFAX: (516) 822-3532

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-085-072-7

Query Match 85.0%; Score 17; DB 4; Length 13;

Best Local Similarity 40.0%; Pred. No. 8.7e+02;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5 |

Db 6 FASSW 10 |

RESULT 2

US-08-469-260A-428
; Sequence 428, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATLAS
; APPLICANT: GEORG J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUREROFF
; APPLICANT: JAMES C. ERICK
; APPLICANT: SHERI L. BULJK
; APPLICANT: ISA K. MUSHARAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/APED
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE: 09-SEP-1993
; PRIORITY APPLICATION DATA:
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-118-270-134
; RESULT 4
; Query Match Score 17; DB 4; Length 34;
; Best Local Similarity 40.0%; Pred. No. 1.7e+03;
; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; Qy 1 FXXXW 5
; Db 16 FTSAW 20
; US-08-118-270-172
; Sequence 172, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A

RESULT 3
US-08-118-270-134
Sequence 134, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A

Query Match Score 17; DB 4; Length 29;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXXW 5
Db 12 FASAW 16

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 172:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-118-270-172

Query Match 85.0%; Score 17; DB 1; Length 34;

Best Local Similarity 40.0%; Pred. No. 1.7e+03; Mismatches 0; Indels 3; Gaps 0;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 16 FTAW 20

RESULT 5 PCT-US93-08528-134

Sequence 134 Application PC/PUS9308528

GENERAL INFORMATION:

APPLICANT: New York University

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

PRIORITY APPLICATION DATA:

FILED DATE: 09-SEP-1993

PRIORITY APPLICATION DATA:

COMPILER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIORITY APPLICATION DATA:

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY=2 PCT

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY=2 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 134:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US93-08528-134

RESULT 6 PCT-US93-08528-172

Sequence 172 Application PC/PUS9308528

GENERAL INFORMATION:

APPLICANT: New York University

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

APPLICATION NUMBER: US 07/943, 236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY=2 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 172:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US93-08528-172

RESULT 7 US-08-467-023-137

Sequence 137 Application US/08467023

PATENT NO: 6090386

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;

APPLICANT: Pollock, Joanne;

APPLICANT: Bond, Julian F.;

APPLICANT: Garman, Richard D.;

APPLICANT: Kuo, Mei-Chang;

APPLICANT: Yeung, Siu-mei H.;

APPLICANT: Brower, Andrew;

APPLICANT: Exley, Mark A.;

APPLICANT: Powers, Steven P.

TITLE OF INVENTION: Allergenic Proteins And Peptides From Japanese Cedar Pollen

TITLE OF INVENTION: Japanese Cedar Pollen

NUMBER OF SEQUENCES: 261

CORRESPONDENCE ADDRESS:

ADDRESSEE: ImmunoLogic Pharmaceutical Corporation, Inc.

STREET: 610 Lincoln St

QY 1 FXXXW 5

Db 16 FTAW 20

CITY: Waltham
 STATE: MA
 COUNTRY: USA
 ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,023
 FILING DATE: June 6, 1995
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/350,225
 FILING DATE: December 6, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Jane E. Remillard
 REGISTRATION NUMBER: 38,872
 REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 137:

SEQUENCE CHARACTERISTICS:
 LENGTH: 36 amino acids

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: Internal

US-08-467-023-137

Query Match 85.0%; Score 17; DB 3; Length 36;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03; Mismatches 0;
 Matches 2; Conservative 0; Indels 0; Gaps 0;

QY	1	FXXXX 5
	1	FXXXX 5
Db	11	FSASW 15

RESULT 8

US-09-330-914A-10
 Sequence 10, Application US/09330914A
 Patent No. 6432671

GENERAL INFORMATION:

APPLICANT: Flöhe, Leopold
 APPLICANT: No. 6432671ecke, Everson
 APPLICANT: Kalisz, Henryk
 APPLICANT: Montemartini, Marisa

TITLE OF INVENTION: TRYPARDOXIN, EXPRESSION PLASMID, PROCESS OF PRODUCTION, METHOD OF USE, TEST KIT, AND PHARMACEUTICAL COMPOSITION

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Brown
 STREET: 233 South Wacker Drive/6300 Sears Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/330 914A
 FILING DATE: 11-Jun-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP97/06983
 FILING DATE: 12-DEC-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, James P.
 REGISTRATION NUMBER: 28,491

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 37 amino acids

TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI SENSE: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-330-914A-10

Query Match 85.0%; Score 17; DB 4; Length 37;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03; Mismatches 0;
 Matches 2; Conservative 0; Indels 0; Gaps 0;

QY	1	FXXXX 5
	1	FXXXX 5
Db	11	FSASW 15

RESULT 9

US-08-467-023-136

Sequence 136, Application US/08467023

PATENT NO. 609386

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;
 APPLICANT: Pollock, Joanne;
 APPLICANT: Bond, Julian F.;
 APPLICANT: Garman, Richard D.;
 APPLICANT: Kuo, Mei-Chang;
 APPLICANT: Yeung, Siu-mei H.;
 APPLICANT: Brauer, Andrew;
 APPLICANT: Exley, Mark A.;
 APPLICANT: Powers, Steven P.;
 TITLE OF INVENTION: Allergenic Proteins And Peptides From
 NUMBER OF SEQUENCES: 261

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
 STREET: 610 Lincoln St
 CITY: Waltham
 STATE: MA
 COUNTRY: USA

ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,023
 FILING DATE: June 6, 1995
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/350,225
 FILING DATE: December 6, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Jane E. Remillard
 REGISTRATION NUMBER: 38,872
 REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 136
 SEQUENCE CHARACTERISTICS: 136

RESULT 10
US-08-467-023-135
Sequence 135, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immulogic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467, 023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350, 225
FILING DATE: December 6, 1994
ATTORNEY /AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025..6 USD2 (IMI-028CRD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-4400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-135

Query Match 85.0%; Score 17; DB 3; Length 45;
Best Local Similarity 40.0%; Pred. No. 2.1e+03; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 33 FSTAW 37

RESULT 11
US-09-149-476-475
Sequence 475, Application US/09149475
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PZ02PL
CURRENT APPLICATION NUMBER: US/09/149, 476
CURRENT FILING DATE: 1998-05-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040, 162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038, 621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040/7, 600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/040/7, 601

EARLIER APPLICATION NUMBER: 60/057, 761
EARLIER FILING DATE: 1997-06-22
EARLIER APPLICATION NUMBER: 60/047, 595
EARLIER APPLICATION NUMBER: 60/047, 599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043, 578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047, 501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043, 670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056, 632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048, 964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061, 060
EARLIER FILING DATE: 1997-10-02

Query Match 85.0% Score 17, DB 4; Length 45;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative; 0; Mismatches 3; Indels

Db 31 FSAAW 35

US-08-118-270-209

Patent No. 5508384
 GENERAL INFORMATION:
 APPLICANT: Murphy, Randall B.
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSE: BROWNY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/118, 270
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943, 236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34, 033
 REFERENCE/DOCKET NUMBER: MURPHY=2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 209:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 49 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US93-08528-209
 Query Match 85.0%; Score 17; DB 1; Length 49;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 QY 1 FXXXW 5
 Db 36 FTSAW 40
 RESULT 14
 US-09-134-001C-4258
 ; Sequence 4258, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Staun et al
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134, 001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064, 964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055, 779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO: 4258
 ; LENGTH: 61
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 ; US-09-134-001C-4258
 RESULT 13
 PCT-US93-08528-209
 ; Sequence 209, Application PC/TUS9308528
 ; GENERAL INFORMATION:
 ; APPLICANT: New York University
 ; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 ; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 ; NUMBER OF SEQUENCES: 348
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: BROWNY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/08528

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Brown
STREET: 223 South Wacker Drive/6300 Sears Tower
CITY: Chicago

STATE: Illinois
COUNTRY: United States of America
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/330,914A

FILING DATE: 11-JUN-1999

CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP97/06983

FILING DATE: 12-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, James P.

REGISTRATION NUMBER: 28,491

REFERENCE/DOCKET NUMBER: 29473/35678

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 80 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: protein

TOPOLogy: linear

HYPOTHETICAL: No

ANTI-SENSE: No

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

; US-09-330-914A-4

Query Match 85.0%; Score 17; DB 4; Length 80;
Best local Similarity 40.0%; Pred. No. 3.1e+03; 3; Indels 0; Caps 0;
Matches 2; Conservative 0; Mismatches 3; ;
QY 1 FXXW 5
|
Db 8 FSASW 12

Search completed: January 29, 2003, 14:12:57
Job time : 16 secs

OM protein - protein search, using sw model

Run on: January 29, 2003, 14:15:53 ; Search time 15 seconds
 (without alignment(s))
 32.045 Million cell updates/sec

Title:	US-003-403-440A-4
perfect score:	20
Sequence:	1 FXXXW 5
scoring table:	BLOSUM62
Searched:	Gapext 0.5
total number of hits satisfying chosen parameters:	3883
Minimum DB seq length:	0
Maximum DB seq length:	20
Post-processing:	Minimum Match 0%
	Maximum Match 100%
Listing first 45 summaries	
Database :	PIR_73:*
1:	pir1:*
2:	pir2:*
3:	pir3:*
4:	pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	17	85.0	9	A24244
2	16	80.0	8	A28004
3	16	80.0	10	A31571
4	15	75.0	8	S10596
5	15	75.0	9	D5744
6	15	75.0	10	T17663
7	15	75.0	10	T12225
8	15	75.0	10	A53789
9	15	75.0	15	PH1613
10	15	75.0	17	A34104
11	15	75.0	20	S7781
12	15	75.0	20	PN0171
13	15	75.0	20	PH1180
14	14	70.0	8	A61348
15	14	70.0	8	S0895
16	14	70.0	8	S0895
17	14	70.0	8	A49823
18	14	70.0	8	B49823
19	14	70.0	8	A44960
20	14	70.0	8	A44960
21	14	70.0	8	A43976
22	14	70.0	8	B43976
23	14	70.0	8	A33995
24	14	70.0	8	S11545
25	14	70.0	8	S55310
26	14	70.0	8	A58620
27	14	70.0	8	A05169
28	14	70.0	10	A60421
29	14	70.0	10	S0895
30	14	70.0	10	2 S0998
31	14	70.0	10	2 A2681
32	14	70.0	10	2 JC416
33	14	70.0	10	2 S0138
34	14	70.0	10	2 B33995
35	14	70.0	10	2 C3191
36	14	70.0	10	2 PT0322
37	14	70.0	10	2 T17066
38	14	70.0	10	2 T17069
39	14	70.0	10	2 T12329
40	14	70.0	12	2 PT0274
41	14	70.0	12	2 PH1324
42	14	70.0	13	2 PC4391
43	14	70.0	16	2 C37290
44	14	70.0	19	2 S32675
45	14	70.0	20	2 PC1240

ALIGNMENTS

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	17	85.0	9	A24244
2	16	80.0	8	A28004
3	16	80.0	10	A31571
4	15	75.0	8	S10596
5	15	75.0	9	D5744
6	15	75.0	10	T17663
7	15	75.0	10	T12225
8	15	75.0	10	A53789
9	15	75.0	15	PH1613
10	15	75.0	17	A34104
11	15	75.0	20	S7781
12	15	75.0	20	PN0171
13	15	75.0	20	PH1180
14	14	70.0	8	A61348
15	14	70.0	8	S0895
16	14	70.0	8	S0895
17	14	70.0	8	A49823
18	14	70.0	8	B49823
19	14	70.0	8	A44960
20	14	70.0	8	A44960
21	14	70.0	8	A43976
22	14	70.0	8	B43976
23	14	70.0	8	A33995
24	14	70.0	8	S11545
25	14	70.0	8	S55310
26	14	70.0	8	A58620
27	14	70.0	8	A05169
28	14	70.0	10	A60421
29	14	70.0	10	S0895

RESULT 1

A24244

adipokinetic hormone - bollworm

N:Alternate names: Hez-AKH

C:Species: Heliotis zea (bollworm, corn earworm, tomato fruitworm)

C:Accession: *#sequence

T.: Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridg

, 622-628, 1986

, structure of a peptide from the corpora cardiaca of Hel

;186794; PMID:3964263

RESULT 2

A28004

adipokinetic hormone G - two-spotted cricket

N:Alternate names: AKH-G

C:Species: Bimaculatus (two-spotted cricket)

C:Accession: 30-Jun-1989 #sequence_revision 24-Oct-1997

C:Accession: A28004

R;Gade, G.; Rinehart, K.L.

Biocat. Biophys. Res. Commun. 149, 908-914, 1987

A:Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide from the corpora cardiaca of the two-spotted cricket, Helicoverpa armigera

A:Reference number: A28004; MUID:8810553; PMID:3426616

A:Accession: A28004

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A;Note: the amino-terminal residue forms pyrrolidine carboxylic acid; therefore, we h

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; Pyroglutamate; F;8;Modified site: amidated carboxyl end (Trp) #status experimental

Query Match Score 80.0%; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
|
4 FSTGW 8

RESULT 3
A31571
hyperrehalosemic/adipokinetic hormone - bollworm
R;Jaffre, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
Biocem. Biophys. Res. Commun. 155, 34-35, 1988
A;Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea w/
C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C;Date: 30-Jun-1989 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C;Accession: A31571
R;Jaffre, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
Biocem. Biophys. Res. Commun. 155, 34-35, 1988
A;Reference number: A31571; MUID:88326324; PMID:3415690
A;Molecule type: protein
A;Residues: 1-10 <AF>
C;Superfamily: adipokinetic hormone
F;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamid
F;10/Modified site: amidated carboxyl end (Asn) #status experimental
F;10/Modified site: amidated carboxyl end (Asn) #status experimental
Query Match 80.0%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
|
Dt 4 FSSGW 8

RESULT 4
S10596
adipokinetic hormone - pond skimmer
C;Species: Libellula auripennis
C;Accession: S10596
R;Raede, G.
Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hc
A;Reference number: S10596; MUID:90359055; PMID:2390213
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: amidated carboxyl end; pyroglutamyl acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (TRP) #status experimental
Query Match 75.0%; Score 15; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
|
Db 4 FTFSW 8

RESULT 5
D57444
neuropeptide Grb-AST B4 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Accession: D57444
R;Jorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: D57444
A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-9 <LOR>
Query Match 75.0%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
|
Db 5 FHGSW 9

RESULT 6
T17063
cytochrome-c oxidase (EC 1.9.3.1) chain I - Hoplocercus spinosus mitochondrion (fragm
C;Species: mitochondrion Hoplocercus spinosus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C;Accession: T17063
R;Macay, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Reference number: 218674; MUID:97315309; PMID:9169559
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U82683; NTID:g3603124; PID:g3603127; PIDN: AAC62284.1
A;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 75.0%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.2e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
|
Db 2 FIRRW 6

RESULT 7
T12325
cytochrome-c oxidase (EC 1.9.3.1) chain I - Leiocephalus carinatus mitochondrion (fra
C;Species: mitochondrion Leiocephalus carinatus
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999
C;Accession: T12325
R;Schulte, J.A.; Macay, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example
A;Reference number: Z17488; MUID:99162288; PMID:10501389
A;Accession: T12325
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-10 <SCB>
A;Cross-references: EMBL:AF049864; NTID:g4105754; PID:g4105757; PIDN: AAD02535.1
A;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 75.0%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.2e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
|
Db 2 FIRRW 6

RESULT 8
S53789
neuropeptide Pec-Hirth - Platypleura capensis

C;Species: Platyleura capensis
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
 C;Accession: S53789
 R;Gaede, G.; Janssens, M.P.E.
 Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
 A;Title: Cicadas contain novel members of the AKH/RPCH family Peptides with hypertrehalose
 A;Reference number: S53789; MUID:95225985; PMID:7710694
 A;Accession: S53789
 A;Molecule type: protein
 A;Residues: 1-10 <GAE>
 C;Keywords: blocked amino end; blocked carboxyl end

Query Match Similarity 75.0%; Score 15; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 4 FSPSW 8

RESULT 9

PH1613
 I9 H chain V-D-J region (clone B-less 17) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;ID: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1613
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609; PMID:8315387
 A;Accession: PH1613
 A;Molecule type: DNA
 A;Residues: 1-15 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match Similarity 75.0%; Score 15; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 10 FTMLW 14

RESULT 10

A34704
 protein-tyrosine kinase (EC 2.7.1.112) 1, neuron-specific - human (fragment)
 C;Species: Homo sapiens (man)
 C;ID: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 04-Feb-2000
 C;Accession: A34704
 R;Myer, J.M.; Bolen, J.B.
 Mol. Cell. Biol. 10, 2035-2040, 1990
 A;Title: Identification of a novel neuronal C-SRC exon expressed in human brain.
 A;Reference number: A34704; MUID:90220588; PMID:1691439
 A;Accession: A34704
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-17 <PY>
 C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match Similarity 75.0%; Score 15; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 1.7e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 10 FTFRW 14

RESULT 11

S77981

cytochrome-c oxidase (EC 1.9.3.1) chain va.1 - bigeye tuna (fragment)
 C;Species: Thunnus obesus (bigeye tuna)
 C;ID: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 26-Feb-1998
 C;Accession: S77981
 R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
 submitted to the Protein Sequence Database, June 1997
 A;Reference number: S77980
 A;Accession: S77981
 A;Molecule type: protein
 A;Residues: 1-20 <ARN>
 A;Experimental source: heart; liver
 C;Genetics:
 A;Genome: nuclear
 C;Function:
 A;Pathway: oxidative phosphorylation; respiratory chain
 C;Superfamily: mammalian cytochrome-c oxidase chain Va
 C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membr

Query Match Similarity 75.0%; Score 15; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 11 FDARW 15

RESULT 12

PN0171
 peptidylprolyl isomerase (EC 5.2.1.8) b, cytosolic - fungus (Fusarium sporotrichoides)
 N;Contains: cyclophilin
 C;Species: Fusarium sporotrichoides
 C;ID: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 02-Sep-2000
 C;Accession: PN0171
 R;Fukaya, N.; Chow, L.-P.; Sugiyama, A.; Ueno, Y.; Tabuchi, K.
 submitted to JIPID, May 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichoides
 A;Reference number: PN0160
 A;Accession: PN0171
 A;Molecule type: protein
 A;Residues: 1-20 <RUK>
 A;Experimental source: strain M-1-1
 C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C;Keywords: cis-trans-isomerase; cyclophilin A binding; cytosol

Query Match Similarity 75.0%; Score 15; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 6 FDITW 10

RESULT 13

PH1380
 alpha-amylase (EC 3.2.1.1) (Haim sensitive) - *Bacillus* sp. (fragment)
 C;Species: *Bacillus* sp.
 C;ID: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 07-May-1999
 C;Accession: PH1380
 R;Kawaguchi, T.; Nada, H.; Murao, S.; Arai, M.
 Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992
 A;Title: Purification and some properties of a Haim-sensitive alpha-amylase from newl
 A;Reference number: PH1380; MUID:93113087; PMID:1369074
 A;Accession: PH1380
 A;Molecule type: protein
 A;Residues: 1-20 <KAW>
 A;Experimental source: strain N0.195
 C;Comment: This enzyme has an optimum pH of 7.0.
 C;Function:
 A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A;Pathway: glycogen/starch degradation
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 75.0%; Score 15; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03; O; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Db 4 FSPNW 8
 Qy 1 FXXXW 5
 C|
 Db 13 FSWTW 17

Search completed: January 29, 2003, 14:17:59
 Job time : 15 secs
 QY 1 FXXXW 5
 |
 Db 4 FSPNW 8

RESULT 14

At:148

red pigment-concentrating hormone - northern shrimp

N; Alternate names: blanching hormone

C; Species: *Pandalus borealis* (northern shrimp)

C; Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C; Accession: A61348; S07139

R; Fernlund, P.; Josefson, L.

Science 177, 173-175, 1972

A; Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.

A; Reference number: A61348; MUID:72228738; PMID:5041363

A; Molecule type: protein

A; Residues: 1-8 <FERR1>

R; Fernlund, P.

Biochim. Biophys. Acta 371, 304-311, 1974

A; Title: Structure of the red-pigment-concentrating hormone of the shrimp, *Pandalus borealis*

A; Reference number: S07139; MUID:75054965; PMID:4433569

A; Molecule type: protein

A; Residues: <FERR2>

A; Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C; Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pigmented pigment-containing cells.

C; Superfamily: adipokinetic hormone

C; Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutam

F; 1; Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

F; 2; Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 70.0%; Score 14; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05; O; Mismatches 0; Indels 0;
 Matches 2; Conservative 0; Db 4 FSPGW 8

RESULT 15

S03995
hypertrehalosemic hormone I - oriental cockroach

N; Alternate names: Pea-CAH-I

C; Species: Blatta orientalis (oriental cockroach)

C; Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997

C; Accession: S03995

R; Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A; Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and the stick insect *Exciatosa tataratum* assigned by tandem fast atom bombard

A; Reference number: S03995; MUID:90253659; PMID:2340112

A; Accession: S03995

A; Molecule type: protein

A; Residues: 1-8 <GAE>

A; Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C; Superfamily: adipokinetic hormone

C; Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F; 1; Modified site: amidated carboxyl end (Trp) #status experimental

F; 2; Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 70.0%; Score 14; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05; O; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Db 4 FSPGW 8

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Gencore version 5.1.3

Run on: January 29, 2003, 14:13:03 ; Search time 10 Seconds

(without alignments)

20.738 Million cell updates/sec

OM protein - protein search, using sw model

Title: US-09-403-440a-4

perfect score: 20

Sequence: 1 FXXXW 5

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1147

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%, Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	16	80.0	8	1	AKHG_GRYBI	P14086 gryllus bimaculatus
2	16	80.0	10	1	HTF_HELZE	P16353 heliothis zea
3	15	75.0	8	1	AKH_LIBAU	P25418 libellula aenea
4	15	75.0	10	1	AKH_LOCMI	P81626 locusta migratoria
5	15	75.0	21	1	COXA_THROB	P80972 thunnius obesus
6	14	70.0	8	1	AKH_TABAT	P14595 tabanus atratus
7	14	70.0	8	1	HTF_PERAM	P04549 periplaneta americana
8	14	70.0	8	1	HTF_BPERAM	P25419 tenebrio molitor
9	14	70.0	8	1	HTF_TEMNO	P08399 pandalus japonicus
10	14	70.0	8	1	RPCH_PANPO	P18110 pomalea micans
11	14	70.0	10	1	HTF1_ROMMI	P11385 carausius marginatus
12	14	70.0	10	1	HTF2_CARMQ	P10939 nauphoeta cornuta
13	14	70.0	10	1	HTF_NAUCT	P14595 tabanus atratus
14	14	70.0	10	1	HTF_TABAT	P4122 photuris luciferina
15	14	70.0	13	1	YPNP_PHOU	P30806 spinacia olarifera
16	13	65.0	6	1	CRTC_SPIOL	P82096 litoria rubra
17	13	65.0	10	1	E101_LITRQ	P04378 petromyzon marinus
18	12	60.0	11	1	GONI_PETMA	P82089 litoria citrina
19	12	60.0	11	1	CA31_LITCI	P82090 litoria citrina
20	12	60.0	11	1	CA32_LITCI	P14595 conus imperialis
21	12	60.0	11	1	OCR3_PERAM	P58649 octopus minor
22	11	55.0	4	1	RPP_BOTIN	P30425 bothrops innoxius
23	11	55.0	5	1	UF01_MOUSE	P38639 mus musculus
24	11	55.0	6	1	LOKL_LOCM1	P41491 locusta migratoria
25	11	55.0	7	1	BRHP_CONIM	P58803 conus imperialis
26	11	55.0	7	1	MYSL_LITRO	P82055 litoria rubra
27	11	55.0	7	1	WWA1_ACHFU	P35919 achatina fulica
28	11	55.0	7	1	WWA2_ACHFU	P35920 achatina fulica
29	11	55.0	7	1	WWA3_ACHFU	P35921 achatina fulica
30	11	55.0	8	1	ACT_THUAL	P18691 thunnius albicans
31	11	55.0	8	1	AKH_MELML	P25423 melolontha hippocastani
32	11	55.0	8	1	CCRN_MACED	P30369 macropus europeus
33	11	55.0	8	1		

ALIGNMENTS

RESULT 1
ID AKHG_GRYBI STANDARD; PRT; 8 AA.
ID AKHG_GRYBI
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
DR MEDLINE=88106553; PubMed=3426616;
DR Rinehart, K.L., Jr.;
DR "Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide with adipokinetic activity from the corpora cardiaca of the cricket Gryllus bimaculatus.";
DR Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RN SEQUENCE.
RC SPECIES=R. microptera; TISSUE=corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede, G., Hilbich, C., Beyreuther, K., Rinehart, K.L., Jr.;
RA "Sequence analyses of two neuropeptides of the AKH/RPCH-family from the Lubber grasshopper, Romalea microptera.";
RT Peptides 9:681-688(1988).
RL CC
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRT / RPCH FAMILY.
DR PIR: A28004; A28004.
DR DR INTERPRO: IPR02047; AKH.
DR PROSITE: PS00256; AKH: 1.
DR Neuropeptide; Amidation; Flight.
FT MOD-RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD-RES 8 8 AMIDATION.
SO SEQUENCE 8 AA: 938 MW: 867861B5B9C452D6 CRC64;

Query Match 80.0%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
RESULT 2
ID HTF_HELZE STANDARD; PRT; 10 AA.
ID HTF_HELZE

AC	PI16353;
DT	01-AUG-1990 (Rel. 15, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	01-FEB-1994 (Rel. 28, Last annotation update)
DE	Hypertrehalosemic hormone (Htz-HRTH).
OS	Heliothis zea (corn earworm) (Bollworm).
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC	Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC	Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.
OK	NCBI_TaxID=7113;
RN	[1]
R2	SEQUENCE.
RC	TISSUE=Corpora cardiaca;
R3	MEDLINE=88322634; PubMed=3415690;
RA	Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
RA	Tseng C.M., Zhang Y.S., Hayes D.K.,
RT	"Isolation and primary structure of a neuropeptide hormone from Heliothis zea with hypertrehalosemic and adipokinetic activities."
RL	Biochem. Biophys. Res. Commun. 195: 344-350(1988).
CC	-!- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC	-!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC	PIR; A31571; A31571.
DR	InterPro; IPR002047; AKH.
DR	PROSITE; PS00256; AKH; 1.
KW	Neuropeptide; Amidation.
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	MOD_RES 10 10 AMIDATION.
SC	SEQUENCE 10 AA; 1096 MW; 8E036765A5B9D1 CRC64;
Query	80.0%; Score 16; DB 1; Length 10; Best Local Similarity 40.0%; Pred. No. 2.9e+02; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db	4 FSSCW 8
RESULT 3	
ID	AKH_LIBAU STANDARD: PRT: 8 AA.
ID	AKH_LIBAU STANDARD: PRT: 8 AA.
AC	P25418;
DT	01-MAY-1992 (Rel. 22, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	01-FEB-1994 (Rel. 28, Last annotation update)
DR	Adipokinetic hormone (AKH).
OS	Libellula auripennis (Skimmer dragonfly).
OC	Eukaryota; Metazoa; Pancrustacea; Hexapoda; Insecta; Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OC	NCBI_TaxID=6966;
RN	[1]
RP	SEQUENCE, AND SYNTHESIS.
RT	TISSUE=Corpora cardiaca;
RT	MDLINE=90359055; PubMed=2390213;
RA	Gaede G.;
RA	"The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone family isolated and sequenced from a dragonfly"; Hope-Seyler 371:475-483 (1990).
RT	-!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
RT	-!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
PIR	PIR; S10506; S10506.
DR	InterPro; IPR002047; AKH.
DR	PROSITE; PS00256; AKH; 1.
Neuopeptide; Amidation; Flight.	
MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.	
MOD_RES 8 8 AMIDATION.	
SQ	SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;
Query	75.0%; Score 15; DB 1; Length 8; Best Local Similarity 40.0%; Pred. No. 1.1e+05; Mismatches 3; Indels 0; Gaps 0;
Matches	2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db	4 FTFSW 8
RESULT 4	
ID	AKH_XLOCMI STANDARD: PRT; 10 AA.
ID	AKH_XLOCMI STANDARD: PRT; 10 AA.
AC	P81626;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Peptide hormone.
OS	Locusta migratoria (Migratory locust).
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
OX	NCBI_TaxID=7004;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=corpora cardiaca;
RA	Sieger K.J.;
RA	Submitted (DEC-1998) to the SWISS-PROT data bank.
RL	CC -!- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.
CC	-!- SIMILARITY: SOME SIMILARITY TO THE AKH / HRTH / RPCH FAMILY.
DR	InterPro; IPR002047; AKH.
DR	PROSITE; PS00256; AKH; 1.
KW	Neuropeptide; Amidation.
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	MOD_RES 10 10 AMIDATION.
SQ	SEQUENCE 10 AA; 1222 MW; 81BPF67AB41B9D1 CRC64;
Query	75.0%; Score 15; DB 1; Length 10; Best Local Similarity 40.0%; Pred. No. 5.1e+02; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db	4 FSRDW 8
RESULT 5	
ID	Coxa.ThuOB STANDARD: PRT; 20 AA.
ID	Coxa.ThuOB STANDARD: PRT; 20 AA.
AC	P80972;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	Cytochrome c oxidase polypeptide Va-1 (BC1.9.3.1) (Fragment).
OS	Thunnus obesus (Bigeye tuna).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Actinopterygii; Teleostei; Neoteleostei; Acanthomorphai; Acanthopterygii; Percomorpha; Perciformes; Scombroidei; Scombridae; Thunnus.
OC	NCBI_TaxID=8241;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Heart, and Liver;
RC	MDLINE=97454291; PubMed=9310366;
RX	"The subunit structure of cytochrome-c oxidase from tuna heart and liver"; Eur. J. Biochem. 248:99-103(1997).
RC	Eur. J. Biochem. 248:99-103(1997).
CC	OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL RESPIRATION;
CC	-!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C

-!- CATALYTIC ACTIVITY: 4 ferrocytocochrome c + 0(2) = 4 ferricytocochrome
 CC C + 2 H(2).O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
 DR InterPro; IPR003204; CYTC_OX5A.
 DR Pfam; PF0224; COXA_1.
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 DR NON_TER 20 AA;
 FT NON_TER 20 AA; 2404 MW; 7E82E43B7157355E CRC64;
 SQ SEQUENCE 20 AA; 2404 MW;

Query Match 75.0%; Score 15; DB 1; Length 20;
 Best Local Similarity 40.0%; Pred. No. 8.6e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXW 5
 Db 11 FDARW 15

RESULT 6

AKH_TABAT	STANDARD;	PRT;	8 AA.
ID	AKH_TABAT		
AC	PI4595;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-FEB-1994 (Rel. 28, Last sequence update)		
DT	01-FEB-1994 (Rel. 28, Last annotation update)		
DE	Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)		
DE	(DCC_I).		
OS	Tabanus atratus (Horse fly).		
OC	Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;		
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;		
OC	Tabanomorpha; Tabanidae; Tabanus.		
OX	NCBI_TaxID=7207;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Corpora cardiaca;		
RX	MEDLINE=90046758; PubMed=2813385;		
RA	Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,		
RA	Vogel V.W., Zhang Y.-S., Hayes D.K.;		
RT	"Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse flies (Diptera);"		
RT	Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).		
RL	-!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.		
CC	-!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.		
DR	PIR; A33995; A33995.		
DR	InterPro; IPR002047; AKH.		
DR	PROSITE; PS00256; AKH_1.		
KW	Neuropeptide; Amidation; Flight.		
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.		
FT	MOD_RES 8 8 AMIDATION;		
SQ	SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;		

Query Match 70.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 Db 4 FPPGW 8

RESULT 7

HTF1_PERAM	STANDARD;	PRT;	8 AA.
ID	HTF1_PERAM		
AC	PO4548;		
DT	13-AUG-1987 (Rel. 05, Created)		
DT	01-FEB-1994 (Rel. 28, Last sequence update)		
DT	01-FEB-1994 (Rel. 28, Last annotation update)		
DE	Hypertrehaloseamic factor I (Neuropeptide M-I) (Periplanetin CC-1)		

Query Match 70.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 Db 4 FPPGW 8

RESULT 8

HTF2_PERAM	STANDARD;	PRT;	8 AA.
ID	HTF2_PERAM		

AC P04549;
 DT 13-AUG-1987 (Rel. 05, created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DF Hypertrehalosaeinic factor III (Neuropeptide M-II) (Periplanetin CC-2)
 DE (Pea-CAH-II) (Teb-CC-II) (Hypertrehalosaeinic neuropeptide M-II) (Periplanetin CC-2)
 OS periplaneta americana (American cockroach),
 OS leptinotarsa decemlineata (Colorado potato beetle), and
 OC Blatta orientalis (oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattoidea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 [1]
 RF SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RZ Witten J.L., Schaffter M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RZ Rinehart K.L.Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 bombardment mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RF SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=64298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 cardioacceleratory and hyperglycemic activity from the corpora
 cardiacia of *Periplaneta americana*";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RF SEQUENCE.
 RC SPECIES=L. decolorlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiacum from the potato
 beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RF SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=230112;
 RA Gaede G., Rinehart K.L.Jr.;
 RT "Primary structures of hypotrehalosaeinic neuropeptides isolated from
 the corpora cardiaca of the cockroaches *Leucophaea maderae*,
Gromphadorhina portentosa, *Blattella germanica* and *Blatta orientalis*
 and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -!- FUNCTION: HYPOTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR A05170; A05170.
 DR S08996; S0896.
 DR B44960; B44960.
 PIR: B44823; B44923.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT SEQUENCE 8 AA; 1005 MW; 8674575B9044735 CR64;
 SQ QY 1 FXXXW 5
 DB 4 FSPNW 8
 RESULT 10
 TD RPCH_PANBO
 AC P08939;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-Oct-2001 (Rel. 40, Last annotation update)
 DE Red pigment concentrating hormone (RPCH).
 OS Pandanus borealis (Northern red shrimp).
 OC Malacostraca; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Caridea; Pandaloidea; Pandalidae; Pandanus.
 OX NCBI_TaxID=6703;
 RN [1]
 RF SEQUENCE.
 RX MEDLINE=75054965; PubMed=4433569;
 RA Fernlund P.;
 RT "Structure of the red-pigment-concentrating hormone of the shrimp
Pandalus borealis";
 RL Biochem. Biophys. Acta 371:304-311(1974).
 CC -!- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY
 CC STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-
 CC CHROMATOPHORES.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR: S07139; S07139.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.

KW Pigment; Hormone; Amidation.
 FT PYRROLIDONE CARBOXYLIC ACID.
 MOD_RES 1 1 AMIDATION.
 SEQUENCE 8 AA; 948 MW; 86786775B9C4736 CRC64;

Query Match 70.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.1e+05; 0; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 4 FSPGW 8

RESULT 11
 HTF1_ROMMI STANDARD; PRT; 10 AA.
 ID HTF1_ROMMI
 AC P18110;
 DT 01-NOV-1990 (Rel. 16, created)
 DT 01-FEB-1994 (Rel. 28, last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE RO I (Hypertrehalosaemic factor).
 OS Romalea microptera (Lubber grasshopper);
 Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Gaeiflora;
 OC Acrideromorpha; Aridoidea; Romaleidae; Romalea.
 OX NCBI_TaxID=7007;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89145002; PubMed=3226548;
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
 RT "Sequence analyses of two neuropeptides of the AKH/RPCh family from
 the Lubber grasshopper, *Romalea microptera*.";
 RL Peptides 9:681-688(1988).
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 THE MAJOR CARBOHYDRATE OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR InterPro; IPR002047; AKH.
 PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight.
 FT PYRROLIDONE CARBOXYLIC ACID.
 MOD_RES 1 1 AMIDATION.
 SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC4;

Query Match 70.0%; Score 14; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 8.8e+02; 0; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 4 FPPNW 8

RESULT 12
 HTF2_CARMO STANDARD; PRT; 10 AA.
 ID HTF2_CARMO
 AC P11385;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hypertrehalosaemic factor II (HTF-II) (HTRH-II) (Hypertrehalosaemic
 neuropeptide II).
 OS Carausius morosus (Indian stick insect), and
 Extatosoma tiaratum (Stick insect).
 OC Eukaryota; Metazoa; Arthropoda; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Phasmatoidea;
 OC Heteroneidiidae; Carausius.
 OX NCBI_TaxID=7022, 7024;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;

RESULT 13
 HTF_NAUCL STANDARD; PRT; 10 AA.
 ID HTF_NAUCL
 AC P10359;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypertrehalosemic hormone (HRTH) (Hypertrehalosaemic neuropeptide).
 OS Nauphoeta cinerea (Cinerous cockroach) (Gray cockroach),
 Leucophaea maderae (Maderia cockroach),
 Blattella germanica (German cockroach), and
 Group phadonia portentosa (Madagascar hissing cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberidae; Blaberidae; Nauphoeta;
 OX NCBI_TaxID=6990, 6988, 6973, 36953;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=N.cinerea; TISSUE=Corpora cardiaca;
 RX MEDLINE=87100208; PubMed=3801028;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Amino acid sequence of a hypertrehalosaemic neuropeptide from the
 corpus cardiacum of the cockroach, *Nauphoeta cinerea*.";
 RL Biochem. Biophys. Res. Commun. 141:774-781(1986).

[2] DR InterPro; IPR002047; AKH.
 RN PROSITE; PS00256; AKH; 1.
 RP SPECIES=L.maderae, G.portentosa, and B.germanica;
 RC MDDLTNP=9073659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "primary structures of hypertrehalosaeamic neuropeptides isolated from
 the corpora cardiaca of the cockroaches *Leucophaea maderae* and *Blatta orientalis*
 and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 atom bombardment mass spectrometry";
 RT Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=B.germanica;
 RX MEDLINE=91179580; PubMed=2080017;
 RA Veenstra J.A., Camps F.;
 RT "Structure of the hypertrehalosaeamic neuropeptide of the German
 cockroach, *Blattella germanica*;"
 RL Neuropeptides 15:107-109(1990).
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE 1S
 THE MAJOR CARBOHYDRATE OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / RTH / RPCH FAMILY.
 DR PIR: A26381;
 DR PIR: S08997; S08997;
 DR PIR: S08998; S08998;
 DR PIR: S09137; S09137;
 DR PIR: A60421; A60421;
 DR Interpro; IPR002047; AKH.
 DR PROSINE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT PYRROLIDONE CARBOXYLIC ACID.
 MOD RES 1 1 AMIDATION.
 SQ 10 AA; 1092 MW; 056236786775B9C4 CRC64;

Query Match Best Local Similarity 70.0%; Score 14; DB 1; Length 10;
 Matches 2; Conservative 0; MisMatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 Db 4 FSPGW 8

RESULT 14 DR SEQUENCE FROM N.A.
 ID STRAINK122;
 RX MEDLINE=94266731; PubMed=8206856;
 RA Clarke D.J.; Dowds B.C.A.;
 RT "The gene coding for polynucleotide phosphorylase in *Photobacter sp.*
 strain K122 is induced at low temperatures.";
 RL J.Bacteriol. 176:3775-3784(1994).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X76069; CA53672.1; -.
 KW Hypothetical protein.
 DT 01-JAN-1990 (Rel. 13, created)
 DT 01-FEB-1994 (Rel. 28, last sequence update)
 DE Hypertrehalosaeamic factor (HOTH) (Dipteran corpora cardiaca factor 11)
 DE (DCC 11).
 OS *Tabanus atratus* (horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Paprustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Tabanomorpha; Tabanidae; Tabanus.
 OC NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptides hormones with adipokinetic and
 RT hypertrehalosaeamic activity isolated from the corpora cardiaca of horse
 flies (Diptera).";
 RL PROC. NATL. ACAD. SCI. U.S.A. 86:8161-8164(1989).
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE 1S
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / RTH / RPCH FAMILY.
 DR PIR; B33995; B33995.

Search completed: January 29, 2003, 14:17:03
 Job time : 10 secs

Run on: January 29, 2003, 14:15:28 ; Search time 28 Seconds
 (without alignments)
 36.794 Million cell updates/sec

OM protein - protein search, using sw model

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GenCore version 5.1.3

title: US-09-403-440A-4
perfect score: 20
Sequence: FXXXW 5

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

- SPTRREMBL_21:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rhodobacter:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	17	85.0	13	8	Q9XL12 benisia tab
2	16	80.0	11	8	Q9G649 otoacryptis
3	16	80.0	17	4	Q9ZT66 hemo sapien
4	16	80.0	19	15	Q9J329 human immun
5	16	80.0	19	15	Q9WB11 human lymfun
6	15	75.0	9	8	Q8W9E6 procambiarus
7	15	75.0	10	8	Q9YF22 leptocephalus
8	15	75.0	10	8	P92707 platysaurus
9	15	75.0	10	8	Q79897 holocercus
10	15	75.0	11	8	Q9G368 draco biline
11	15	75.0	8	8	Q9G646 silvana pont
12	15	75.0	11	8	Q9C643 calotes cal
13	15	75.0	11	8	Q9G640 calotes cey
14	15	75.0	11	8	Q9G634 calotes lio
15	15	75.0	11	8	Q9G631 calotes nig
16	15	75.0	11	8	Q9G365 calotes emm

ALIGNMENTS

RESULT 1

ID	Q9XL12	PRELIMINARY;	PRT;	13 AA.
AC	Q9XL12;			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Cytochrome oxidase I (Fragment).			
OS	Benisia tabaci (Sweetpotato whitefly).			
OG	Mitochondrion.			
RA	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleurodidae; Aleyrodoidea; Aleyrodidae; Aleyrodinae; Benisia.			
RT	"A phylogeographical analysis of the Benisia tabaci species complex based on mitochondrial DNA markers.";			
RL	Mol. Ecol. 8:1583-1591 (1999).			
DR	EMBL: AF110703; AAD28415.1; -.			
KW	Mitochondrion.			
FT	NON_TER	1	1	
SQ	SEQUENCE	13 AA:	1639 MW:	8DD68729F5744365 CRC64;
Query	Match		85.0 %;	Score 17; DB 8; Length 13;
Matches	Best Local Similarity	40.0 %;	Pred. No. 8.2e+02;	Indels 0; Gaps 0
QY	1	FXXXW 5		
Db	3	FTSSW 7		

RESULT 2

ID	Q9G649	PRELIMINARY;	PRT;	11 AA.
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09G649;	RESULT 4
LT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
LT	01-MAY-2001 (TREMBLrel. 16, Last annotation update)
LE	Cytochrome c oxidase subunit I (Fragment).
GN	otocryptis wiegmanni.
CS	Mitochondrion.
CG	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepiosauria; Squamata; Iguania; Acrodontia; Agamidae; Draconinae; Otopterygia; Otoptychidae; Lizards.
CC	NCBI_TaxID=118220;
OC	[1]
OX	RNA
RN	SEQUENCE FROM N.A.
RA	Macev J.R., Schulte J.A. II, Larson A.; "Evolution and information content of the mitochondrial genomic structural features illustrated with acrodont lizards"; Syst. Biol. 49:257-277(2000). [2]
RT	SEQUENCE FROM N.A.
RA	Macev J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y., Petriyagoda R., Restegar-Pouyan N., Papenfuss T.J.; "Evaluating Trans-Tethys migration: An example using Acrodont lizard phylogenetics"; Syst. Biol. 49:233-256(2000).
DR	EMBL: AF128480; AAC00677.1; -.
KW	Mitochondrion.
RA	NON_TER 11
FT	SEQUENCE 11 AA; 1347 MW; 932D3710D3640DC1 CRC64;
Qy	1 FXXXW 5
Db	3 FTARW 7
RESULT 3	
015276	
ID	015276 PRELIMINARY; PRT; 17 AA.
AC	015276; TREMBLrel. 05, created
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DB	Mitochondrial translation elongation factor EF-Tu (Fragment).
TM	TUFM.
OC	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;	[1]
RNA	SEQUENCE FROM N.A.
RA	Jacobs H.T., Smurthwaite L., Koshy R.; "Human genomic sequences encoding mitochondrial elongation factor EF-Tu: Evidence for post-endosymbiotic intron insertion"; Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RT	EMBL: Y11797; CAA72493.1; -.
RL	Elongation factor.
RR	NON_TER 1
FT	SEQUENCE 17 AA; 2019 MW; BF737D12D2AB0ATE CRC64;
Qy	1 FXXXW 5
Db	1 FSLRW 5
RESULT 4	
09J329	PRELIMINARY; PRT; 19 AA.
ID	09J329 PRELIMINARY; PRT; 19 AA.
AC	09J329; TREMBLrel. 08, Created
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Envelope glycoprotein (Fragment).
GN	Human immunodeficiency virus type 1.
OC	Viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11676;
RN	[1]
RA	SEQUENCE FROM N.A.
RT	MEDLINE=98285741; PubMed=9621043;
RA	Bielic L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L., Safar M., Barre-Sinoussi F., Kazatchkine M.D.; "Genetically related human immunodeficiency virus type 1 in three adults of a family with no identified risk factor for intrafamilial transmission"; J. Virol. 72:5831-5839(1998).
RL	EMBL: U87216; AAC32976.1; -.
DR	AIDS; Coat protein; Glycoprotein.
KW	NON_TER 1
FT	SEQUENCE 19 AA; 2294 MW; 3781714A9E073911 CRC64;
Qy	1 FXXXW 5
Db	10 FNSTW 14

AC 0BWE65;
DT 01-MAR-2002 (TREMBrel. 20, Created)
DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Procambarus clarkii (Red swamp crayfish).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocymemata; Astacidae;
OC Astacoidea; Cambaridae; Procambaridae.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE FROM N.A.
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
Cunningham C.W.;
RT "Mitochondrial gene rearrangements support a hypothesis of parallel evolution to the crab-like form.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF436024; AAC31599.1; -.
KW MITOCHONDRION.
FT NON_TER 1 1
SEQUENCE 9 AA; 1185 MW; 936BB9C733640321 CRC64;
Query Match 75.0%; Score 15; DB 8; Length 9;
Best Local Similarity 40.0%; Pred. No. 6 7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXXW 5
Db 1 FTRW 5

RESULT 7
ID 092YT2 PRELIMINARY; PRT; 10 AA.
AC 092YT2; 01-MAY-1999 (TREMBrel. 10, Created)
DT 01-MAY-1999 (TREMBrel. 10, Last sequence update)
DE CYTOCHROME C OXIDASE SUBUNIT I (Fragment).
GN COI.
OS Leiocephalus carinatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguanidae; Tropidurinae;
OC Leiocephalidae;
OX NCBI_TaxID=81825;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162288; PubMed=10051389;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: A general procedure and example using four subfamilies of the lizard family Iguanidae.";
RL Mol. Phylogenet. Evol. 10:367-376(1998).
DR EMBL; AF049864; AAC02535.1; -.
KW Mitochondrion.
FT NON_TER 10 10
SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;
Query Match 75.0%; Score 15; DB 8; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXXW 5
Db 2 FITRW 6

RESULT 8
ID P92707 PRELIMINARY; PRT; 10 AA.
AC P92707;

RESULT 9
ID 079897 PRELIMINARY; PRT; 10 AA.
AC 079897; 01-NOV-1998 (TREMBrel. 08, Created)
DT 01-NOV-1998 (TREMBrel. 08, Last sequence update)
DR 01-NOV-1998 (TREMBrel. 08, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (Fragment).
GN COI.
OS Hoplocercus spinosus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguanidae; Hoplocercinae;
OC Hoplocercus.
OX NCBI_TaxID=52193;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97315309; PubMed=9169559;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Evolutionary shifts in three major structural features of the mitochondrial genome among iguanian lizards.";
RL J. Mol. Evol. 14:660-674(1997).
DR EMBL; U82683; AAC62284.1; -.
KW Mitochondrion.
FT NON_TER 10 10
SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;
Query Match 75.0%; Score 15; DB 8; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXXW 5
Db 2 FITRW 6

RESULT 10
 O9G368 PRELIMINARY; PRT; 11 AA.
 ID O9G368;
 AC 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DI Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OG Draco blanfordii.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosaurs; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Draco.
 NCBI_TaxID=89021;
 RI [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=97153810; PUBMED=9000751;
 RZ Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary
 structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 RM [2]
 SEQUENCE FROM N.A.
 RZ Macey J.R., Schulze J.A., II, Larson A., Ananjeva N.B., Wang Y.,
 RT "Evolution and information content of the mitochondrial genomic
 structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [3]
 SEQUENCE FROM N.A.
 RA Macey J.R., Schulze J.A., II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL: AF128477; AACG00668.1; -.
 KW Mitochondrion.
 FT NON_TER 11 AA; 1341 MW; 4B2D371E336415B7 CRC64;
 SEQUENCE 11 AA; 75.0%; Score 15; DB 8; Length 11;
 Query Match Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 DB 3 FLSRW 7

RESULT 11
 Q95646 PRELIMINARY; PRT; 11 AA.
 ID Q95646;
 AC 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Sitana ponticeriana.
 OG Mitochondrion.
 OC Euryoya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Sitana.
 NCBI_TaxID=118235;
 RI [1]
 SEQUENCE FROM N.A.
 RA Macey J.R., Schulze J.A., II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL: AF128482; AACG00683.1; -.
 KW Mitochondrion.
 FT NON_TER 11 AA; 1373 MW; BE2D371E336411A6 CRC64;
 SEQUENCE 11 AA; 75.0%; Score 15; DB 8; Length 11;
 Query Match Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 DB 3 FMTRW 7

RESULT 12
 O9G643 PRELIMINARY; PRT; 11 AA.
 ID O9G643;
 AC 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DI Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Calotes calotes.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosaurs; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Calotes.
 NCBI_TaxID=118093;
 RI [1]
 SEQUENCE FROM N.A.
 RA Macey J.R., Schulze J.A., II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 SEQUENCE FROM N.A.
 RA Macey J.R., Schulze J.A., II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL: AF128482; AACG00683.1; -.
 KW Mitochondrion.
 FT NON_TER 11 AA; 1373 MW; BE2D371E336411A6 CRC64;
 SEQUENCE 11 AA; 75.0%; Score 15; DB 8; Length 11;
 Query Match Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 DB 3 FMTRW 7

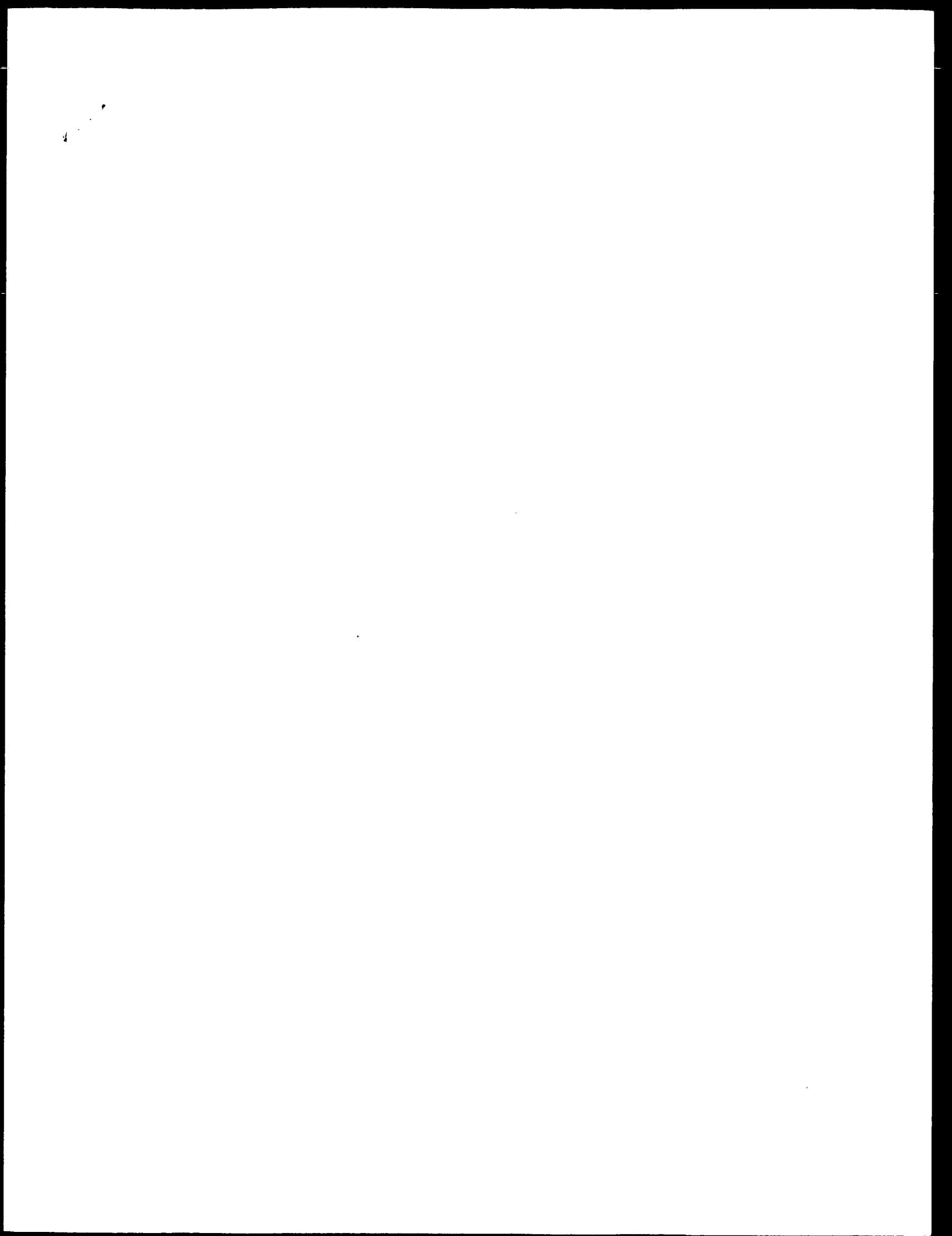
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Leptidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Calotes.
 OX NCBI_TaxID=118094;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macey, J.R., Schulte, J.A., II, Larson A.; Ananjeva N.B., Wang Y.,
 RT "Evolution and information content of the mitochondrial genomic
 structural features illustrated with acrodont lizards.",
 RT Syst. Biol. 49:257-277(2000).
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128483; AAG00686; 1; -.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Macey, J.R., Schulte, J.A., II, Larson A., Ananjeva N.B., Wang Y.,
 RT "Evolution and information content of the mitochondrial genomic
 structural features illustrated with acrodont lizards.",
 RT Syst. Biol. 49:257-277(2000).
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macey, J.R., Schulte, J.A., II, Larson A., Ananjeva N.B., Wang Y.,
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics.",
 RT Syst. Biol. 49:233-256(2000).
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128486; AAG00695; 1; -.
 KW Mitochondrion.
 FT NON_TER 11 11 MW; 4B2D371E336411A7 CRC64;
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;
 Query Match 75.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 3 FLTRW 7

RESULT 14

Q9G634 PRELIMINARY; PRT; 11 AA.

ID Q9G634
 AC 09G634
 DT 01-MAR-2001 (TREMBLrel. 16, created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 RL 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Calotes liolepis.
 OC Osteichthyes.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Calotes.
 OX NCBI_TaxID=118096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macey, J.R., Schulte, J.A., II, Larson A.; Ananjeva N.B., Wang Y.,
 RT "Evolution and information content of the mitochondrial genomic
 structural features illustrated with acrodont lizards.",
 RT Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Macey, J.R., Schulte, J.A., II, Larson A., Ananjeva N.B., Wang Y.,
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics.",
 RT Syst. Biol. 49:233-256(2000).
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128485; AAG00692; 1; -.
 KW Mitochondrion.
 FT NON_TER 11 11 MW; 4B2D371E336411A7 CRC64;
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;
 Query Match 75.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 Db 3 FLTRW 7

Search completed: January 29, 2003, 14:17:38
 Job time : 29 secs



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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 29, 2003, 14:12:43 ; Search time 34 seconds
 (without alignments)
 19.596 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXXW 5

Scoring table: BIOSEARCH62

Gapopen 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 289567

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%, Listing first 45 summaries

Database :

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- 1: /SIDS2/gcgdata/geneseq/geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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- 10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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- 18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	17	85.0	10 21 AAB0010	H. pylori beta ure
2	17	85.0	10 22 AAB86058	H. pylori beta ure
3	17	85.0	10 22 AAB86090	H. pylori beta ure
4	17	85.0	13 22 AAED0735	Complementarity-de
5	17	85.0	14 22 AAM98088	Human peptide #136
6	17	85.0	15 17 AAR97874	Japan cedar pollen
7	17	85.0	15 17 AAR97875	Japan cedar pollen
8	17	85.0	15 19 AAW57758	Residues 16-30 of
9	17	85.0	19 23 AAE23038	Human thioredoxin, T-cell epitope pep
10	17	85.0	20 19 AAW2165	

ALIGNMENTS

RESULT 1

ID AAB10010
XX AAB10010 standard; Protein: 10 AA.

AC AAB10010;

XX DT 01-NOV-2000 (first entry)

XX DE H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.

XX KW Acid-resistant microorganism; detection; faecal; intestine; infection;

KW monoclonal antibody; heavy chain; complementarity determining region;

KW CDR; beta-urease.

XX OS Unidentified.

XX PN WO20026671-A1.

XX PD 11-MAY-2000.

XX PF 29-OCT-1999; 99WO-EP08212.

XX PR 29-OCT-1998; 98EP-0120517.

XX PR 06-NOV-1998; 98EP-0120687.

XX PA (CONN-) CONNEX GMBH.

XX PI Reiter C, Culmann G, Friedrichs U, Heppner P, Lakner M;

PI Ringlis A;

XX DR WPI: 2000-365747/31.

DR N-PSB; AAA40166.

Complementarity de
 Fusion immunoglobu
 Histamine/serotonin
 Immunogenic peptid
 Human secreted tum
 N. meningitidis LO
 Sequence of new go
 Example of gonadot
 Human CASP618 prot
 Human CASB618 prot
 Human APT-186 tryp
 Breast-cancer asso
 Murine PSA antibody
 Anti-NKG2D hybrido
 N. meningitidis LO
 Human Factor V pro
 Promiscuous T help
 Universal helper T
 Pan-DR binding pep
 Pan DR-binding pep
 Padre (pan-DR bind
 Pan DR epitope pep
 Cladosporium herba
 Human peptide #177
 Human peptide #208
 Antigenic Polypept
 SP120 peptide 110.
 Fusion immunoglobu
 Ganglioside GM1-bu
 Peptide #8. Unde

PT Detecting infection by acid-fast microbes for diagnosis of helicobacter
 PT pylori, comprises reacting a faecal sample with two binding reagents for
 CC antigens that survive intestinal passage

XX Claim 26; Page 22; 84pp; German.

CC This invention describes a novel method for the detection of a mammalian
 CC infection by an acid-resistant microorganism (A) by treating a faecal
 CC sample with at least two different monoclonal antibodies (Mab) (or their
 CC fragments or derivatives) or aptamers (collectively (I)) and detecting for
 CC formation of a complex (C) between (I) and the corresponding antigen of
 CC (A). The first and second (I) bind to epitopes of different antigens
 CC (Ag). These epitopes are present, after passage through the intestines,
 CC in at least some mammals, and have either: (i) their native structure;
 CC or (ii) a structure against which an antibody is produced by an animal
 CC infected or immunized with (A), or its extract, lysate, derived protein
 CC or fragment, or with a synthetic peptide. Practically all mammals display
 CC at least one of the specified epitopes. The method is used to detect
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
 CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepatica,
 CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
 CC therapeutically. The method is direct and non-invasive, and provides an
 CC inexpensive and easily standardizable diagnosis, despite possible
 CC degradation of antigens during passage through the intestines. This
 CC sequence represents a fragment of a H. pylori beta-urease-binding
 CC antibody heavy chain complementarity determining region (CDR1) which is
 XX used to illustrate the method of the invention.

Sequence 10 AA;

Query Match 85.0%; Score 17; DB 21; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 DR: 4 FSTSW 8

RESULT 2
 AAB86058
 ID AAB86058 standard; Peptide: 10 AA.

XX AAB86058;
 XX DT 17-JUL-2001 (first entry)

DE H. pylori beta-urease derived antibody light chain CDR1 #1.
 XX

KW Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
 KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;
 KW antibacterial; complementarity determining region.

OS Unidentified.
 XX

PN WO200127613-A2.

XX PD 19-APR-2001.

XX P1 12-OCT-2000; 2000WO-EP10058.

XX PR 12-OCT-1999; 99EP-0120351.

PR 16-MAR-2000; 2000EP-0105592.

PR 31-MAR-2000; 2000EP-0107028.

PR 10-MAY-2000; 2000EP-0110110.

PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

XX PI Reiter C., Cullmann G., Heppner P., Ringveis A., Mueller H., Haindl E.;
 XX DR WPI; 2001-282087/29.

XX DR N-PSDB; AAF88060.

PT Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
 CC sample

XX PS Claim 23; Page 17; 89pp; German.

CC This invention describes a novel method for detecting in a mammal,
 CC infection by an acid-resistant microorganism (A) which comprises reacting
 CC a fecal sample with: (i) a receptor (R) such that a complex is formed
 CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
 CC complex is formed with Ag, and the formation of a complex detected. R are
 CC specific for an Ag which, after passage through the intestines, at least
 CC in some mammals, retains a native (or corresponding) structure against
 CC which the mammal produces antibodies (when immunized or infected with
 CC (A), or its extracts, lysates or derived proteins (or fragments) or
 CC synthetic peptides). The products of the invention have antibacterial
 CC activity. The method is used to diagnose infection by Helicobacter,
 CC campylobacter or Mycobacterium, particularly H. pylori (most preferred),
 CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the
 CC progress of treatment. Receptors, particularly antibodies, directed
 CC against Ag can be used therapeutically for treatment of infections. The
 CC method requires only one R to provide a reasonably secure diagnosis
 CC (although use of two R improves sensitivity), so it is relatively
 CC inexpensive and more easily standardized. Also, it is direct,
 CC non-invasive, suitable for automation and may indicate the stage of an
 CC infection. This sequence represents a complementarity determining region
 CC (CDR) from an antibody generated against a Helicobacter pylori antigen
 CC (catalase or beta-urease) which is used to illustrate the method of the
 CC invention.

XX SQ Sequence 10 AA;

Query Match 85.0%; Score 17; DB 22; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03; Gaps 0;

CC Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 DR 4 FSTSW 8

RESULT 3
 AAB86090
 ID AAB86090 standard; Peptide: 10 AA.

XX AAB86090;
 XX DT 17-JUL-2001 (first entry)

DE H. pylori beta-urease derived antibody light chain CDR1 #1.

KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
 KW acid-resistant microorganism; complementarity determining region;

KW CDR; feces; heavy chain; light chain.

OS Unidentified.
 XX

PN WO200127612-A2.

XX PD 19-APR-2001.

XX P1 12-OCT-2000; 2000WO-EP10057.

XX PR 12-OCT-1999; 99EP-0120351.

PR 16-MAR-2000; 2000EP-0105592.

PR 31-MAR-2000; 2000EP-0107028.

PR 10-MAY-2000; 2000EP-0110110.

PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

XX PI Reiter C., Cullmann G., Laktion M., True A., Dehnert S., Schwartz G.;

XX DR WPI; 2001-282086/29.

DR N^{*}PSDB: AAF88117.
 XX detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing *Helicobacter pylori*, comprises immunochromatographic
 PT detection of antigen in feces -
 XX
 PS Claim 27; Page 27; 90pp; German.

This invention describes a novel method for detecting infection by an acid-resistant microorganism (A), in a mammal, using immunochromatographic assay. The method is used to diagnose infection by an acid-resistant microorganism (A), in a mammal, such as *Helicobacter*, *Campylobacter* or *Mycobacterium*, particularly *H. pylori* (most preferred), *H. hepatica*, *C. Jejuni* and *M. tuberculosis*. The method is rapid, simple, inexpensive and non-invasive, and may indicate the stage of infection. A test strip used in the method may include a filter to eliminate particles present in the sample and only a single receptor provides a reasonably secure diagnosis with specificity and selectivity improved by detecting several epitopes (of catalase) or different antigens (catalase and beta-urease). The method can be automated. This sequence represents a complementarity-determining region (CDR) from an antibody raised against the *H. pylori* catalase or beta-urease antigen which is used to illustrate the method of the invention.

SQ Sequence 10 AA;

Query Match 85.0%; Score 17; DB 22; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0; MisMatches 3; Dbs 4; FSTSW 8

QY 1 FXXW 5
 4 FSTSW 8

RESULT 4
 AAE05735

ID AAE05735 standard; peptide; 13 AA.
 XX
 KW AAE05735;

AC
 XX
 DT 24-SEP-2001 (first entry)

DE Complementarity-determining region 3 (CDR3) of MoPhabs #7.
 XX
 KW CDR3; complementarity-determining region 3; monoclonal phage antibody; MoPhabs; antigen.

XX
 OS Synthetic.
 XX
 PN US6265150-B1.
 XX
 PR 24-JUL-2001.

XX
 PF 26-MAY-1998; 98US-0085072.
 XX
 PR 07-JUN-1995; 95US-0483633.
 PR 18-SEP-1997; 97US-0932892.

XX
 PA (BECT) BECTON DICKINSON & CO.
 PA (CRUC-) CRUCELL HOLLAND BV.
 PT Terstappen LW, Logtenberg T;
 XX
 DR WPI; 2001-463929/50.

XX
 PT Obtaining a phage particle, useful for obtaining human antibodies
 PT against known and novel surface antigens, by incubating a phage library
 PT with target cells to allow binding of the antibody fragment to the
 PT antigen.

XX
 PS Example 6; Column 6; 6pp; English.

CC The invention relates to a method of obtaining a phage particle
 CC which has an antibody fragment directed against an antigen associated
 CC with the surface of target cells in a heterogeneous cell population.
 CC The method involves incubating a library of phage particles with the
 CC target cells to allow binding of the antibody fragment expressed on
 CC the surface of the phage particles to the antigen associated with
 CC the target cells. The method is useful for obtaining human antibodies
 CC expressed on phenotypically defined subpopulations of cells.
 CC The present sequence is complementary-determining region 3 (CDR3)
 CC of monoclonal phage antibodies (MoPhabs) used in the exemplification
 CC of the invention.

XX
 SQ Sequence 13 AA;

RESULT 5
 RAM98088

ID RAM98088 standard; Peptide; 14 AA.
 XX
 DE Human peptide #1363 encoded by a SNP oligonucleotide.
 XX
 AC RAM98088;

DT 24-JAN-2002 (first entry)

XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiopoietin; apoptosis related protein; Cadherin; factor;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.

XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.

XX
 PD 05-JUL-2001.

XX
 PF 28-DEC-2000; 2000WO-US35498.

XX
 PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

XX
 PA (CURA-) CURAGEN CORP.

XX
 PI Shimkets RA, Leach M.

XX
 DR WPT; 2001-465210/50.

XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

XX
 PS Disclosure; Page 3967; 4143pp; English.

XX
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinases, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioestersases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.

The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g., rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system and an infection of pathogenic organisms.

Sequence 14 AA:

Query Match 85.0%; Score 17; DB 22; Length 14;
Best Local Similarity 40.0%; Pred. No. 2.e+03; Mismatches 0;
Matches 2; Conservative 0; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 6 FASTW 10

RESULT 6
ID AAR97874
XX AAR97874 standard; peptide; 15 AA.
AC AAR97874;
DT 16-AUG-1996 (first entry)
DF Japan cedar pollen mature allergen Cry j II amino acids 16-30.
XY Allergen; epitope; overlapping peptide; cry j II; cedar pollen;
KW Sugi pollinosis; diagnosis; treatment.
XY Cryptomeria japonica.
OS Cryptomeria japonica.

PN JP08047392-A.
XX PR 20-FEB-1996.
XX PR 07-NOV-1994; 94JP-0297840.
XX PR 26-MAY-1994; 94JP-0134868.
XX PR 05-NOV-1993; 93JP-0276773.
XX PA (MEIP) MEIJI MILK PROD CO LTD.
DR WPI: 1996166249/17.
XX PT Japan cedar pollen allergen Cry j II epitope - comprises at least
PT part of specified 460 amino acid protein
XX PS Claim 8; Fig 3; 17pp; Japanese.
XX CC AAR97871-R97960 are overlapping peptides used for the epitope mapping
CC of the Japan cedar pollen allergen Cry j II. cry j II and allergenic
CC peptides of it are useful in the diagnosis, prevention and treatment
CC of Sugi pollinosis, the allergic reaction to Japan cedar pollen.
CC Significant regions of the allergen were identified using the
CC overlapping peptides of the full epitope derived from a Cry j II
CC antigen-specific T cell line. Amino acids 66-80 (AAR97884) and 186-200
CC (R978908) of the full mature 460 amino acid allergen are the most
XX allergenic of the 90 peptides tested.

Sequence 15 AA:

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+03; Mismatches 0;
Matches 2; Conservative 0; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 4 FASTW 8

RESULT 7
ID AAR97875
XX AAR97875 standard; peptide; 15 AA.
AC AAR97875;
DT 16-AUG-1996 (first entry)

DE Japan cedar pollen mature allergen Cry j II amino acids 21-35.
XX KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
XX Cryptomeria japonica.

PN JP08047392-A.
XX PR 20-FEB-1996.
XX PR 07-NOV-1994; 94JP-0297840.
XX PR 26-MAY-1994; 94JP-0134868.
XX PR 05-NOV-1993; 93JP-0276773.
XX PA (MEIP) MEIJI MILK PROD CO LTD.
DR WPI: 1996166249/17.

XX PT Japan cedar pollen allergen Cry j II epitope - comprises at least
PT part of specified 460 amino acid protein
XX PS Claim 8; Fig 3; 17pp; Japanese.

XX CC AAR97871-R97960 are overlapping peptides used for the epitope mapping
CC of the Japan cedar pollen allergen Cry j II. cry j II and allergenic
CC peptides of it are useful in the diagnosis, prevention and treatment
CC of Sugi pollinosis, the allergic reaction to Japan cedar pollen.
CC Significant regions of the allergen were identified using the
CC overlapping peptides of the full epitope derived from a Cry j II
CC antigen-specific T cell line. Amino acids 66-80 (AAR97884) and 186-200
CC (R978908) of the full mature 460 amino acid allergen are the most
XX allergenic of the 90 peptides tested.

Sequence 15 AA:

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+03; Mismatches 0;
Matches 2; Conservative 0; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 4 FASTW 8

RESULT 8
ID AAW57758
XX AAW57758 standard; peptide; 15 AA.
AC AAW57758;
DT 17-SEP-1998 (first entry)
DE Residues 16-30 of Cry j 2.
XX
XX CRY J 2; Japanese cedar pollen antigen; allergy; immunotherapy;
KW HLA class II molecule.
XX OS Cryptomeria japonica.
XX PN W99820902-A1.

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+03; Mismatches 0;
Matches 2; Conservative 0; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 9 FASTW 13

PT New human thioredoxin nucleic acid and polypeptide molecules,
 PD 22-MAY-1998.
 XX designated 22108 and 47916, useful for diagnosing, preventing or
 PT treating cancer (e.g. carcinoma), cardiovascular diseases (e.g. heart
 PF failure) or brain disorders -
 XX
 PR 13-NOV-1996; 96JPP-0302053.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 PI Dairiki K, Kino K, Kume A, Sone T;
 XX
 DR WPI; 1998-297617/26.
 XX
 PT Peptides derived from Japanese cedar pollen antigens are
 PT immunotherapeutic agents - useful for allergy treatment and typing
 PT HLA class II molecules in allergy sufferers
 XX
 PS Claim 12; Page 29; 50pp; Japanese.
 XX
 CC This sequence represents residues 16-30 of the Cry j 2 protein, and
 CC is a peptide of the invention. The peptides are derived from Japanese
 CC cedar pollen antigens and are used as immunotherapeutic agents in the
 CC treatment of allergy. The peptides can be used for identification and
 CC typing of the particular HLA class II molecules in an allergy sufferer,
 CC and also for peptide immunotherapy of an allergy. Using these peptides
 CC the immunotherapy can be targeted more specifically to the requirements
 CC of the individual patient, allowing more effective treatment of an
 CC allergy, including those patients for whom treatment with a conventional
 CC immunotherapeutic agent is ineffective.
 XX
 SQ Sequence 15 AA:
 Query Match 85.0%; Score 17; DB 19; Length 15;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 9 FSQAW 13
 RESULT 9
 AAE23038 standard; peptide; 19 AA.
 ID AAE23038;
 AC AAE23038;
 DT 21-AUG-2002 (first entry)
 XX
 DE Human thioredoxin, 47916 peptide.
 XX
 KW Human; thioredoxin; 23108; 47916; haematopoietic disorder; leukaemia;
 KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
 KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
 KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
 KW cytostatic; carcinoma; cardiant; neuroprotective; antiinflammatory;
 KW gene therapy; nootropic.
 OS Homo sapiens.
 XX
 PN WO200224803-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 25-SEP-2001; 2001WO-US29967.
 XX
 PR 25-SEP-2000; 2000US-235049P.
 XX
 PA (MILL-) MILLENIUM PHARM INC.
 XX
 PI Bandaru R, Kapeller-Libermann R;
 XX
 DR WPI; 2002-416475/44.
 XX
 PT T-cell epitope peptide portion of Japanese cypress pollen antigens
 PT PT Chao1 and Chao2 - used for diagnosis and treatment of spring tree
 PT pollen disease
 XX
 PS Claim 2; Page 36; 71pp; Japanese.
 XX
 CC The present sequence represents a T-cell epitope peptide from Japanese
 CC cypress pollen antigen Chao2. The present invention describes peptides
 CC which correspond to the T-cell epitope sites on Japanese cypress pollen
 CC antigens Chao1 and Chao2. The peptides can be used as a reagent for the
 CC diagnosis of allergy to Japanese cypress pollen, and as an antigen in

PT Disclosure; Page 11; 124pp; English.
 CC The invention relates to human thioredoxin nucleic acid and polypeptide
 CC molecules, designated 22108 and 47916. The compound that modulates the
 CC activity or expression of 22108 and 47916 nucleic acid is useful for
 CC treating or preventing a disorder characterised by aberrant activity of
 CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting
 CC the aberrant activity of the 22108 and 47916-expressing cell. The
 CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
 CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,
 CC metastatic or haemato poetic disorders (e.g. leukaemia), or cancers of
 CC the lung, breast, thyroid, head neck, prostate or genito-urinary tract),
 CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
 CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
 CC disease). The thioredoxin DNA is also useful in gene therapy. The
 CC present sequence is human thioredoxin, 47916 peptide.
 XX
 SQ Sequence 19 AA:
 Query Match 85.0%; Score 17; DB 23; Length 19;
 Best Local Similarity 40.0%; Pred. No. 2.5e+03; Mismatches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 4 FSQAW 8
 RESULT 10
 AAW42165 standard; peptide; 20 AA.
 ID AAW42165
 AC AAW42165;
 DT 16-JUN-1998 (first entry)
 XX
 DE T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
 XX
 KW Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
 KW diagnosis; allergy; spring tree pollen disease; pollinosis.
 XX
 OS Chamaeyparis obtusa.
 XX
 PN WO9747548-A1.
 XX
 PD 18-DEC-1997.
 XX
 PF 12-JUN-1997; 97WO-JP02031.
 XX
 PR 14-JUN-1996; 96JPP-0153527.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 PI Dairiki K, Kino K;
 XX
 DR WPI; 1998-052242/05.
 XX
 PT T-cell epitope peptide portion of Japanese cypress pollen antigens
 PT PT Chao1 and Chao2 - used for diagnosis and treatment of spring tree
 PT pollen disease
 XX
 PS Claim 2; Page 36; 71pp; Japanese.

CJ the treatment and prevention of spring tree pollen disease in which the
 CC pollinosis involves reactivity to Japanese cypress pollen.
 XX

Sequence	20 AA;	Matches	2;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
SQ		OY	1	FXXXW	5						
		Db	4	FSSSW	8						

Query Match_b 85.0%; Score 17; DB 19; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.6e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 Db 4 FSSSW 8

QY 1 FXXXW 5
 Db 8 FAWTW 12

RESULT 11

AAG62999 standard; peptide; 20 AA.

XX AAG62999;
 AC XY
 01-OCT-2001 (first entry)

XX Complementarity determining region 3 (CDR3) of VH chain of clone G101.

XY Antibody; light chain; VL; amyloid protein; blood brain barrier;
 KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
 KW transferrin receptor; neurological disease; Alzheimer's disease;
 KW prion disease; AIDS-related dementia; epilepsy; brain injury.

XX Homo sapiens.

XZ OS MUS SP.
 PK OS Homo sapiens.

XX PN WO9856087-A1.

PF XX PD 20-APR-1998.

XX PR 13-FEB-1998; 98WO-US02766.

XX PR 13-FEB-1997; 97US-0040581.

XX PA (AMNIA-) AMERICAN NAT RED CROSS.

XX PI Scott D, Zambidis E;
 XX DR WPI; 1998-506315/43.

XX PT New fusion immunoglobulin heavy chain including gp120 epitopes and
 PT related complete antibodies - DNA, vectors and transformed cells,
 PT used to induce tolerance to the epitopes for treatment of human
 PT immune deficiency virus infection

PS Disclosure; Page 40; 154PP; English.

XX This sequence is an epitope used in the construction of a novel fusion
 CC immunoglobulin heavy chain (IgH) protein with a mammalian, especially
 CC human, IgH chain fused in frame at its N-terminus to one or more human
 CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or
 CC transfected cells are used to tolerate subjects to gp120 epitopes and to
 CC maintain this tolerance, particularly for treatment of HIV infection, and
 CC optionally together with other therapeutic/prophylactic agents such as
 CC vaccines, chemotherapeutic agents and immune response modifiers. Such
 CC proteins can be used against other diseases where an immune response is
 CC deleterious, e.g. microbial infection, tumours or autoimmune disease.
 CC Induction of tolerance suppresses production of antibodies against gp120,
 CC so prevents or inhibits bystander, apoptosis of uninfected T cells that
 CC are bound to gp120 protein, maximising induction of protective antiviral
 CC T cell immunity.

XX SQ Sequence 6 AA;

Query Match 80.0%; Score 16; DB 19; Length 6;
 Best Local Similarity 40.0%; Pred. No. 7.7e+05; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
 Db 2 FNSTW 6

Query Match Similarity 85.0%; Score 17; DB 22; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.6e+03;

QY 1 FXXXW 5
 Db 8 FAWTW 12

RESULT 13

XX	Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC: HLA;
AY18082	KW immune response; T cell activation; major histocompatibility complex;
ID AY18082	KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX	KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
AC AY18082;	KW vaccine; immunisation.
XX	OS Synthetic.
DE Histamine/serotonin cyclic binding peptide.	OS Homo sapiens.
XX	XX
XX	Histamine binding protein; serotonin binding compound; inflammation;
KW	gastric acid secretion; allergy; type I hypersensitivity reaction;
KW	asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy;
KW	drug allergy; respiratory disease; psychological disorder; vaccine;
KW	respiratory disease; coronary heart disease; cellular growth regulator;
XX	tissue repair; blood-sucking ectoparasite; therapy.
OS Synthetic.	XX
XX	OS
PN WO927104-A1.	XX
XX	XX
PD 03-JUN-1999.	XX
XX	XX
PP 26-NOV-1998;	98WO-GB03530.
XX	XX
PR 26-JUN-1998;	98GB-0013917.
PR 26-NOV-1997;	97GB-0025046.
XX	XX
PA (OXFO-) OXFORD VACS LTD.	DR 16-SEP-1999.
XX	XX
PT Nuttall PA, Paesen GC;	PR 13-MAR-1998;
XX	98WO-US05039.
DR WPI; 1999-357841/30.	XX
XX	XX
PT Histamine and serotonin binding compounds useful for the treatment	PS 13-MAR-1998;
PT of allergies	PA (EPM-) EPIMMUNE INC.
XX	XX
PS Claim 9; Page 43; 84pp; English.	PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX	XX
This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking ectoparasites.	WPI; 1999-551214/46.
XX	XX
SQ Sequence 8 AA:	PT New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
Query Match 80.0%; Score 16; DB 20; Length 8;	XX
Best Local Similarity 40.0%; Pred. No. 7.7e+05; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	PS Claim 1; Page 136; 150pp; English.
OY 1 FXXXW 5	XX
Db 4 FAEAN 8	XX
SQ Sequence 9 AA;	XX
Query Match 80.0%; Score 16; DB 20; Length 9;	XX
Best Local Similarity 40.0%; Pred. No. 7.7e+05; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	XX
OY 1 FXXXW 5	XX
Db 5 FFSSW 9	XX
SQ Sequence 9 AA;	XX
Query Match 80.0%; Score 16; DB 20; Length 9;	XX
Best Local Similarity 40.0%; Pred. No. 7.7e+05; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	XX
OY 1 FXXXW 5	XX
Db 5 FFSSW 9	XX
RESULT 15	XX
AAE01057	XX
ID AAE01057 standard; peptide; 9 AA.	XX
XX	XX
AC AAE01057;	XX
XX	XX
DT 17-JUL-2001 (first entry)	XX
XX	XX
DE Human secreted tumour antigen 36P6D5 peptide #10.	XX
XX	KW Human; 36P6D5 protein; secreted tumour antigen; therapy; cancer; kidney;
DE Immunogenic peptide having a human leukocyte antigen binding motif #2695.	KW

KW
KW
MHC; major histocompatibility complex; human leucocyte antigen; HLA-A2.
XX
OS
Homo sapiens.

XX
PN
WO200131015-A2.

XX
PD
03-MAY-2001.

XX
PF
30-OCT-2000; 2000WO-US29894.

XX
PR
28-OCT-1999; 99US-0162417.

PA
(UROG -) UROGENESYS INC.

XX
PI
Raitano AB, Jakabovits A, Faris M, Afar DEH, Hubert RS;

XX
DR
WPI; 2001-308646/32.

XX
PT
Detecting presence of cancer expressing 36P65 protein in individual by
PT comparing protein level in test sample to normal sample, where elevated
level of protein in test sample indicates presence of cancer

XX
PS
Claim 18; Page 91; 113pp; English.

CC
The present invention relates to a gene and its encoded secreted tumour
CC antigen, termed 36P65. These sequences are used for the diagnosis and
CC treatment of various cancers which express 36P65, such as cancers of
CC the kidney, bladder, ovary, breast, pancreas, colon and lungs. In normal
CC individuals 36P65 protein, is predominantly expressed in pancreas, with
CC lower levels of expression in prostate and small intestine. Vaccines, with
CC comprising immunogenic protein of 36P65 is useful for inhibiting the
CC development of prostate or colon cancer. Pharmaceutical composition
CC comprising 36P65 protein is useful for diagnosis and/or prognosis of
CC prostate cancer and other cancers, for modulating or inhibiting the
CC expression of 36P65 genes and/or translation of the 36P65 transcripts,
CC and as therapeutic agents. The present sequence is human 36P65 peptide.
CC This sequence binds to the human MHC (major histocompatibility complex)
CC class I molecule (human leucocyte antigen) HLA-A2 and its half time of
CC dissociation is 9.7

XX
SQ
Sequence 9 AA;

Query Match	Score	DB	Length	9;
Best Local Similarity	80.0%	DB 22;		
Matches	40.0%	Pred. No.	7.7e+05;	
Ov	2;	Mismatches	0;	
Db	1 FXXXXW 5	Indels	3;	
	4 FRSSW 8	Gaps	0;	

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Job time : 35 secs

OM protein - protein search, using sw model

Run on: January 29, 2003, 14:17:43 ; Search time 11 Seconds
 (without alignments)
 9.172 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 12226 seqs, 2017851 residues

Total number of hits satisfying chosen parameters: 36068

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0*, Maximum Match 10*

Listing first 45 summaries

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 3: /cgn2_6/ptodata/1/pupbaa/US06_NEW_PUB.pep; *
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 11: /cgn2_6/ptodata/1/pupbaa/US10_PUBCOMB.pep; *
 12: /cgn2_6/ptodata/1/pupbaa/US60_NEW_PUB.pep; *
 13: /cgn2_6/ptodata/1/pupbaa/US60_PUBCOMB.pep; *
 14: /cgn2_6/ptodata/1/pupbaa/US60_PUBCOMB.pep; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	16	80.0	7	9	US-10-046-922-48	Sequence 48, Appl
2	16	80.0	7	9	US-03-771-639-284	Sequence 284, Appl
3	16	80.0	9	9	US-10-046-922-59	Sequence 59, Appl
4	16	80.0	10	9	US-09-826-290-453	Sequence 453, Appl
5	16	80.0	13	9	US-03-949-375A-18	Sequence 18, Appl
6	16	80.0	13	9	US-03-785-215-19	Sequence 19, Appl
7	16	80.0	13	10	US-09-894-018-69	Sequence 69, Appl
8	16	80.0	15	10	US-09-205-658-284	Sequence 284, Appl
9	16	80.0	18	10	US-09-205-658-283	Sequence 283, Appl
10	16	80.0	18	10	US-09-205-658-285	Sequence 285, Appl
11	16	80.0	19	10	US-09-864-761-415A6	Sequence 415A6, Appl
12	16	80.0	20	10	US-09-812-528-19	Sequence 19, Appl
13	16	80.0	20	10	US-09-884-441-411	Sequence 441, Appl
14	16	80.0	20	10	US-09-884-441-412	Sequence 442, Appl
15	15	75.0	6	9	US-09-486-734A-34	Sequence 34, Appl
16	15	75.0	6	10	US-09-214-371-83	Sequence 83, Appl
17	15	75.0	6	10	US-09-734-384-4	Sequence 4, Appl
18	15	75.0	6	10	US-09-734-384-5	Sequence 5, Appl
19	15	75.0	12	US-10-155-059-1	Sequence 1, Appl	

ALIGNMENTS

RESULT 1
 US-10-046-922-48
 Sequence 48, Application US-10046922
 ; Sequence 284, Application US-09774639
 ; Patent No. US20020164667A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alitalo, Kari
 ; ATTORNEY: Koivunen, Erkki
 ; APPLICANT: Kubo, Hajime
 ; TITLE OF INVENTION: 3 INHIBITOR MATERIALS AND METHODS
 ; FILE REFERENCE: 28967/3708A
 ; CURRENT APPLICATION NUMBER: US-10/046,922
 ; CURRENT FILING DATE: 2002-01-15
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 48
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: peptide

US-10-046-922-48

Query Match Best Local Similarity 80.0%; Score 16; DB 9; Length 7;
 Matches 2; Conservative 40.0%; Pred. No. 9.9e+04; Mismatches 3; Indels 0; Gaps 0;

QY	1	FXXXW 5	2	EENAW 7	Db	3

; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 90 Human Secreted Proteins
 ; FILE REFERENCE: P2013P1
 ; CURRENT APPLICATION NUMBER: US/09774,639
 ; CURRENT FILING DATE: 2001-07-09
 ; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
 ; PRIORITY FILING DATE: EARLIER FILING DATE: 1999-02-04
 ; NUMBER OF SEQ ID NOS: 371

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ_ID NO: 284
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-774-639-284

Query Match          80.0%; Score 16; DB 9; Length 7;
Best Local Similarity 40.0%; Pred. No. 9.9e+04; Mismatches 3;
Matches 2; Conservative 0; Indels 0; Gaps 0;

Qy      1 FXXXW 5
Db      2 FGTSW 6

RESULT 3
US-10-046-922-59
; Sequence 59, Application US/10046922
; Patent No. US2002164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046, 922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 9
; TYPE: PRT
; ORGANISM: peptide
; US-10-046-922-59

Query Match          80.0%; Score 16; DB 9; Length 9;
Best Local Similarity 40.0%; Pred. No. 9.9e+04; Mismatches 3;
Matches 2; Conservative 0; Indels 0; Gaps 0;
Qy      1 FXXXW 5
Db      4 FEAAW 8

RESULT 4
US-09-826-290-453
; Sequence 453, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826, 290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194, 504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253, 647
; PRIOR FILING DATE: 2000-11-28

Query Match          80.0%; Score 16; DB 9; Length 7;
Best Local Similarity 40.0%; Pred. No. 9.9e+04; Mismatches 3;
Matches 2; Conservative 0; Indels 0; Gaps 0;

Qy      1 FXXXW 5
Db      1 FSGTW 5

RESULT 5
US-09-949-375A-18
; Sequence 18, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949, 375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic amino acid sequence of SEQ ID NO: 17.
; US-09-949-375A-18

Query Match          80.0%; Score 16; DB 9; Length 13;
Best Local Similarity 40.0%; Pred. No. 5.9e+02; Mismatches 3;
Matches 2; Conservative 0; Indels 0; Gaps 0;
Qy      1 FXXXW 5
Db      3 FVAAW 7

RESULT 6
US-09-785-215-19
; Sequence 19, Application US/09785215
; Publication No. US20020181715A1
; GENERAL INFORMATION:
; APPLICANT: JENSEN, Martin Roland et al.
; TITLE OF INVENTION: NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID
; FILE REFERENCE: 3631-0107P
; CURRENT APPLICATION NUMBER: US/09/785, 215
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial T-cell epitope capable of binding to a large portion
; OTHER INFORMATION: of MHC Class II molecules in a variety of animals
; US-09-785-215-19

Query Match          80.0%; Score 16; DB 9; Length 13;
Best Local Similarity 40.0%; Pred. No. 5.9e+02; Mismatches 3;
Matches 2; Conservative 0; Indels 0; Gaps 0;
Qy      1 FXXXW 5

```

RESULT 7 ; 3 FVAAW 7 Db

; Sequence 69, Application US/09894018
; Patent No. US2002119127A1

GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Dennis
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033-00
; CURRENT APPLICATION NUMBER: US/09/894 018
; CURRENT FILING DATE: 2001-06-27
; PRIORITY NUMBER: PCT/US00/35568
; PRIORITY FILING DATE: 2000-12-28
; PRIORITY APPLICATION NUMBER: US 60/173, 390
; PRIORITY FILING DATE: 1999-12-28
; PRIORITY APPLICATION NUMBER: US 60/284, 221
; PRIORITY FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE sequence
; US-09-894-018-69

Query Match 80.0%; Score 16; DB 10; Length 13;
Best Local Similarity 40.0%; Pred. No. 5.9e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXXW 5
Db 3 FVAAW 7

RESULT 8 ; US-09-205-658-284

; Sequence 284, Application US/09205658
; Patent No. US20010029617A1

GENERAL INFORMATION:
; APPLICANT: Ruvkin, Gary
; APPLICANT: Ruvkin, Gary
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205, 658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857, 076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888, 534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans

Query Match 80.0%; Score 16; DB 10; Length 18;
Best Local Similarity 40.0%; Pred. No. 7.3e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXXW 5
Db 12 FSTRW 16

RESULT 9 ; US-09-205-658-283

; Sequence 283, Application US/09205658
; Patent No. US20010029617A1

GENERAL INFORMATION:
; APPLICANT: Ruvkin, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205, 658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857, 076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888, 534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans

Query Match 80.0%; Score 16; DB 10; Length 18;
Best Local Similarity 40.0%; Pred. No. 7.3e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXXW 5
Db 9 FSTRW 13

RESULT 10 ; US-09-205-658-285

; Sequence 285, Application US/09205658
; Patent No. US20010029617A1

GENERAL INFORMATION:
; APPLICANT: Ruvkin, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205, 658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857, 076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888, 534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: 08/888, 534
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans

Query Match 80.0%; Score 16; DB 10; Length 18;
Best Local Similarity 40.0%; Pred. No. 7.3e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXXW 5

RESULT 11		RESULT 12	
Qy	Db	Qy	Db
1 FXXXW 5	15 FSHSW 19	1 FXXXW 5	15 FSHSW 19
<p>US-09-864-761-4154 6 ; Sequence 41546, Application US/09864761 ; Patent No. US2009048763A1 ; GENERAL INFORMATION: ; APPLICANT: Penn, Sharron G. ; APPLICANT: Rank, David R. ; APPLICANT: Harrel, David K. ; APPLICANT: Chen, Weisheng ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ; FILE REFERENCE: Neomica-X-1 ; CURRENT APPLICATION NUMBER: US/09/864,761 ; CURRENT FILING DATE: 2001-05-23 ; PRIOR APPLICATION NUMBER: US 60/1780,312 ; PRIOR FILING DATE: 2000-02-04 ; PRIOR APPLICATION NUMBER: US 60/207,456 ; PRIOR FILING DATE: 2000-05-26 ; PRIOR APPLICATION NUMBER: US 09/632,366 ; PRIOR FILING DATE: 2000-08-03 ; PRIOR APPLICATION NUMBER: GB 24263,6 ; PRIOR FILING DATE: 2000-10-04 ; PRIOR APPLICATION NUMBER: US 60/236,359 ; PRIOR FILING DATE: 2000-09-27 ; PRIOR APPLICATION NUMBER: PCT/US01/00666 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00667 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00664 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00669 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00665 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00668 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00663 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00662 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00661 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: PCT/US01/00670 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR APPLICATION NUMBER: US 60/234,687 ; PRIOR FILING DATE: 2000-09-21 ; PRIOR APPLICATION NUMBER: US 09/608,408 ; PRIOR FILING DATE: 2000-06-30 ; PRIOR APPLICATION NUMBER: US 09/774,203 ; PRIOR FILING DATE: 2001-01-29 ; NUMBER OF SEQ ID NOS: 49117 ; SOFTWARE: Aanomax Sequence Listing Engine vers. 1.1 ; SEQ ID NO 41546 ; LENGTH: 19 ; TYPE: PRT ; ORGANISM: Homo sapiens ; FEATURE: ; OTHER INFORMATION: MAP TO AL139352, 8 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9 </p>			
<p>US-09-812-528-19 ; Sequence 19, Application US/09812528 ; Patent No. US20010018210A1 ; GENERAL INFORMATION: ; APPLICANT: Bachovchin, William ; APPLICANT: Wallner, Barbara ; TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN ; VITRO ; FILE REFERENCE: I0248/7015 ; CURRENT APPLICATION NUMBER: US/09/812,528 ; CURRENT FILING DATE: 2001-03-20 ; PRIOR APPLICATION NUMBER: US 60/060,306 ; PRIOR FILING DATE: 1997-09-29 ; PRIOR APPLICATION NUMBER: US 09/162,934 ; PRIOR FILING DATE: 1998-09-29 ; NUMBER OF SEQ ID NOS: 20 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 19 ; LENGTH: 20 ; TYPE: PRT ; ORGANISM: homo sapiens ; US-09-812-528-19 </p>			
<p>Query Match 80.0% Score 16; DB 10; Length 20; Best Local Similarity 40.0%; Pred. No. 7.8e+02; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 FXXXW 5 Db 3 FASRW 7 </p>			
<p>RESULT 13 US-09-884-441-411 ; Sequence 411, Application US/09884441 ; Patent No. US20020119158A1 ; GENERAL INFORMATION: ; APPLICANT: Agate, Paul A. ; APPLICANT: Carter, Darick ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ; DIAGNOSIS OF OVARIAN CANCER ; FILE REFERENCE: 210121:462C7 ; CURRENT APPLICATION NUMBER: US/09/884,441 ; CURRENT FILING DATE: 2001-06-18 ; NUMBER OF SEQ ID NOS: 489 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 411 ; LENGTH: 20 ; TYPE: PRT ; ORGANISM: Homo sapiens ; US-09-884-441-411 </p>			
<p>Query Match 80.0% Score 16; DB 10; Length 20; Best Local Similarity 40.0%; Pred. No. 7.8e+02; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 FXXXW 5 Db 11 FAISW 15 </p>			
<p>RESULT 14</p>			

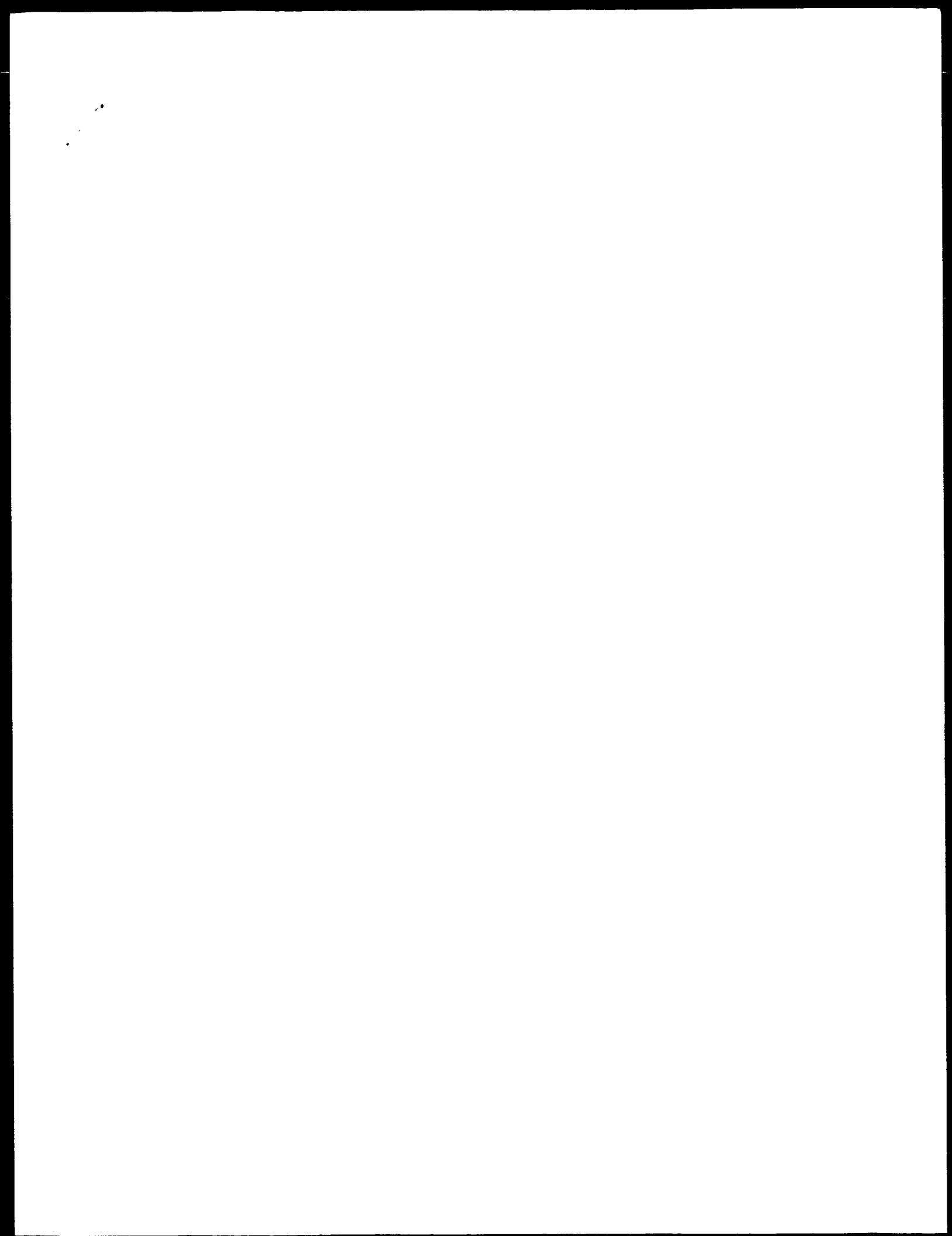
Patent No. US2002011918A1
 GENERAL INFORMATION:
 APPLICANT: Algate, Paul A.
 APPLICANT: Carter, Darren
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.462C/
 CURRENT APPLICATION NUMBER: US/09/884,441
 CURRENT FILING DATE: 2001-06-18
 NUMBER OF SEQ ID NOS: 489
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 412
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-884-441-412

Query Match 80.0%; Score 16; DB 10; Length 20;
 Best Local Similarity 40.0%; Pred. No. 7.8e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXW 5
 |
 Db 4 FAISW 8

RESULT 15
 US-09-486-734A-34
 Sequence 34, Application US/09486734A
 ; Patent No. US2002011918A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chopin, Marie-Christine
 ; APPLICANT: Clier, Florence
 ; APPLICANT: Erlich, S. Dusko
 ; APPLICANT: Gautier, Michel
 ; APPLICANT: Schouler, Catherine
 ; APPLICANT: Institut National de la Recherche Agronomique
 ; TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
 ; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
 ; FILE REFERENCE: 33339/196048
 ; CURRENT APPLICATION NUMBER: US/09/486,734A
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: PCT/FR98/01873
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: FR 97/10885
 ; PRIOR FILING DATE: 1997-09-02
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 34
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: HisdS subunit
 ; US-09-486-734A-34

Query	Match	75.0%	Score	15;	DB	9;	Length	6;	
	Best Local Similarity	40.0%	Pred. No.	9.9e+04;					
Matches	2;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	FXXXW	5						
Db	1	FADDW	5						

Search completed: January 29, 2003, 14:21:23
 Job time : 12 secs



Om protein - protein search, using sw model

Run on: January 29, 2003, 14:16:53 ; Search time 134 Seconds
 (without alignments)
 24.057 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXXW 5

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 4569144 seqs, 64473310 residues

Total number of hits satisfying chosen parameters: 694069

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%, Maximum Match 100%
 Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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ALIGNMENTS

RESULT 1
 US-10-072-419-3 ; Sequence 3, Application US/10072419
 ; GENERAL INFORMATION:
 ; APPLICANT: Schacter, Bernice
 ; APPLICANT: Schacter, Lee
 ; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in H
 ; FILE REFERENCE: 10739-1
 ; CURRENT APPLICATION NUMBER: US/10/072,419
 ; CURRENT FILING DATE: 2002-02-07
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Apis mellifera

US-10-072-419-3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	17	85.0	9	US-10-072-419-3
2	17	85.0	9	US-10-072-419-8
3	17	85.0	10	US-09-843-776A-28
4	17	85.0	10	US-10-089-452-36
5	17	85.0	10	US-10-110-410-36
6	17	85.0	11	US-10-072-419-37

SUMMARIES

Qy	1 FXXXW 5	Db	4 FTSSW 8
Matches 2;	Conservative	0;	Mismatches 3;
Indels 0;	Gaps 0;		

RESULT 2
 US-10-072-419-8

Sequence 8, Application US/10072419
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human Cells
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-072-419-8

Query Match 85.0%; Score 17; DB 24; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.2e+06; 0; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mis 3; In 0; Gap 0;

Qy 1 FXXXW 5
Db 4 FTSW 8

RESULT 3
US-09-842-776A-28
; Sequence 28, Application US/09842776A
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; TITLE OF INVENTION: IN THE STOOL
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR) of an antibody heavy chain directed to a beta-threase
; OTHER INFORMATION: antibody heavy chain directed to a beta-threase
; OTHER INFORMATION: epitope (alternative sequence)
; OTHER INFORMATION: Description of Artificial Sequence: CDR

Query Match 85.0%; Score 17; DB 24; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.2e+06; 0; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mis 3; In 0; Gap 0;

Qy 1 FXXXW 5
Db 4 FTSW 8

RESULT 5
US-10-110-410-35
; Sequence 35, Application US/10110410
; GENERAL INFORMATION:
; APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
; TITLE OF INVENTION: Immunochromatographic Rapid Test for Detecting Acid Resistant Microorganisms in the Stool
; FILE REFERENCE: D 1805 PCT
; CURRENT APPLICATION NUMBER: US/10/110,410
; CURRENT FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Description of Artificial Sequence: CDR

Query Match 85.0%; Score 17; DB 25; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.6e+04; 0; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mis 3; In 0; Gap 0;

Qy 1 FXXXW 5
Db 4 FTSW 8

RESULT 6
US-10-072-419-37
; Sequence 37, Application US/10072419
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human Cells
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-072-419-37

Query Match 85.0%; Score 17; DB 24; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.7e+04; 0; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mis 3; In 0; Gap 0;

Qy 1 FXXXW 5
Db 4 FTSW 8

RESULT 7
US-09-355-397C-36
; Sequence 36, Application US/09355397C

; GENERAL INFORMATION:
; APPLICANT: Spyrou, Giannis
; TITLE OF INVENTION: Mammalian Thioredoxin
; FILE REFERENCE: 102043-100
; CURRENT APPLICATION NUMBER: US/09/355,397C
; CURRENT FILING DATE: 1999-10-18
; PRIORITY NUMBER: PCT/GB98/00263
; PRIORITY FILING DATE: 1998-01-28
; PRIORITY APPLICATION NUMBER: GB 9801710.7
; PRIORITY FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: mammal
; US-09-355-397C-36

Query Match 85.0%; Score 17; DB 17; Length 14;
Best Local Similarity 40.0%; Pred. No. 2e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; MisMatches 0;

Qy 1 FXXXW 5
Db 5 FSATW 9

RESULT 8
US 09-308-027-12
; Sequence 12, Application US/09308027
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Kosuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENTTM
; FILE REFERENCE: 05501/031001
; CURRENT APPLICATION NUMBER: US/09/308,027
; CURRENT FILING DATE: 1999-08-16
; PRIORITY NUMBER: PCT/JP97/04129
; PRIORITY FILING DATE: 1997-11-12
; PRIORITY APPLICATION NUMBER: JP 8/302053
; PRIORITY FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027-12

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; MisMatches 0;

Qy 1 FXXXW 5
Db 9 FSATW 13

RESULT 9
US-09-308-027-88
; Sequence 88, Application US/09308027
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Kosuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENTTM
; FILE REFERENCE: 05501/031001
; CURRENT APPLICATION NUMBER: US/09/308,027A
; CURRENT FILING DATE: 1999-08-16
; PRIORITY NUMBER: PCT/JP97/04129
; PRIORITY FILING DATE: 1997-11-12
; PRIORITY APPLICATION NUMBER: JP 8/302053
; PRIORITY FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 15

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; MisMatches 0;

Qy 1 FXXXW 5
Db 4 FSTAW 8

RESULT 10
US-09-308-027A-12
; Sequence 12, Application US/09308027A
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Kosuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENTTM
; FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308,027A
; CURRENT FILING DATE: 1999-08-16
; PRIORITY NUMBER: PCT/JP97/04129
; PRIORITY FILING DATE: 1997-11-12
; PRIORITY APPLICATION NUMBER: JP 8/302053
; PRIORITY FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027A-12

Query Match 85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; MisMatches 0;

Qy 1 FXXXW 5
Db 9 FSATW 13

RESULT 11
US-09-308-027A-88
; Sequence 88, Application US/09308027A
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Kino, Kosuke
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENTTM
; FILE REFERENCE: 06501/031001
; CURRENT APPLICATION NUMBER: US/09/308,027A
; CURRENT FILING DATE: 1999-08-16
; PRIORITY NUMBER: PCT/JP97/04129
; PRIORITY FILING DATE: 1997-11-12
; PRIORITY APPLICATION NUMBER: JP 8/302053
; PRIORITY FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 15

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; TYPE: PRT
; ORGANISM: Cryptomeria
; US-09-308-027A-88

Query Match          85.0%; Score 17; DB 17; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+04; 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3;
Db      1 FXXXW 5
Dd      4 FSATW 8

RESULT 12
US-09-963-339-10
; Sequence 10, Application US/09963339
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
; FILE REFERENCE: 10448-090001
; CURRENT APPLICATION NUMBER: US/09/963, 339
; PRIORITY APPLICATION NUMBER: 60/235, 049
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-963-339-10

RESULT 13
US-10-145-586-59
Query Match          85.0%; Score 17; DB 23; Length 19;
Best Local Similarity 40.0%; Pred. No. 2.4e+04; 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      1 PXXXW 5
Db      4 FSATW 8

RESULT 14
US-09-202-464-45
Sequence 45, Application US/09202464
; GENERAL INFORMATION:
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: T-CELL, EPITOPE PEPTIDES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/09/202, 464
; APPLICATION NUMBER: US/09/202, 464
; FILING DATE: 14-Dec-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO JPP97/02031
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: JP 8/153527
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., Janis K.
; REGISTRATION NUMBER: 34,819
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
; US-09-202-464-45

Query Match          85.0%; Score 17; DB 16; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.5e+04; 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      1 FXXXW 5
Db      8 FATTW 12

RESULT 15
US-09-240-203B-265
Sequence 265, Application US/09240203B
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.; Pollock, Joanne; Bond, Julian F.; Garman, Richard D.; Kuo, Mei-Chang; Powers, Steven P.; Exley, Mark A.; Chen, Xian; Shaked, Ze'ev
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; NUMBER OF SEQUENCES: 265
; US-10-145-586-59

Query Match          85.0%; Score 17; DB 25; Length 19;
Best Local Similarity 40.0%; Pred. No. 2.4e+04; 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
TYPE: PRT
ORGANISM: Homo sapiens
; US-10-145-586-59

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• CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield, LLP
STREET: 28 State St
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,203B
FILING DATE: 22-Jun-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994

ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragoras, Esq.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

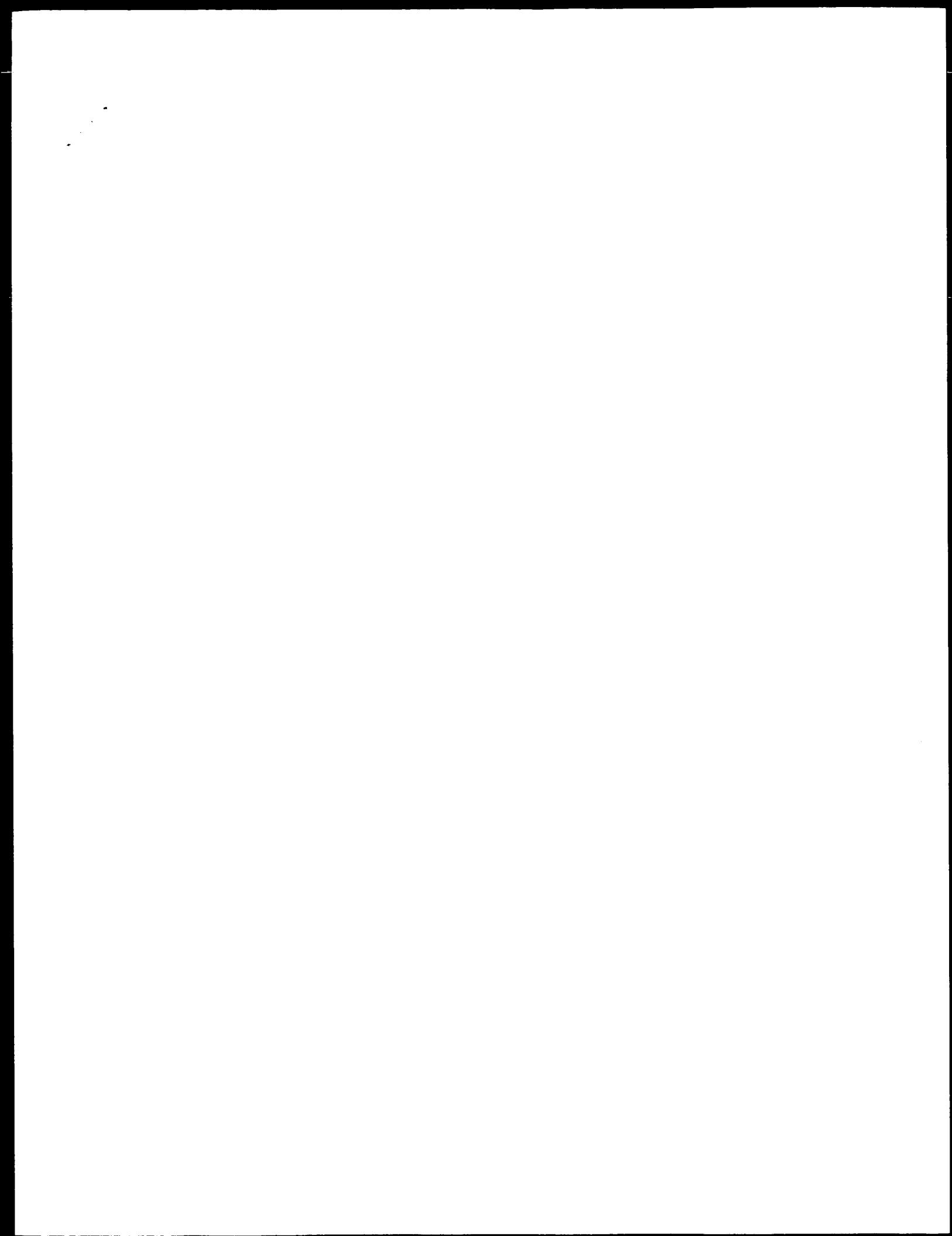
FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US - 09 - 240 - 203B - 265

Query Match 85.0%; Score 17; DB 16; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 FXXW 5
|
Db 12 FSTAW 16

Search completed: January 29, 2003, 14:20:41
Job time : 135 secs



PRIOR APPLICATION NUMBER: US 60/172,705
 PRIORITY FILING DATE: 1999-12-10
 NUMBER OF SEQ ID NOS: 51504
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 21722
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide Derived from Human Papillomavirus

US-09-641-528-21722
 Query Match 80.0%; Score 16; DB 5; Length 8;
 Best Local Similarity 40.0%; Pred. No. 3e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;
 Qy 1 FXXXXW 5
 Db 1 FSRTW 5

RESULT 7
 US-09-641-528-21757
 Sequence 21757, Application US/09641528
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Chesnut, Robert
 APPLICANT: Celis, Esteban
 APPLICANT: Grey, Howard
 TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
 TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
 FILE REFERENCE: 2060_010001
 CURRENT APPLICATION NUMBER: US/09/641,528
 CURRENT FILING DATE: 2000-08-15
 PRIOR APPLICATION NUMBER: US 60/172,705
 PRIOR FILING DATE: 1999-12-10
 NUMBER OF SEQ ID NOS: 51504
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 21757
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide Derived from Human Papillomavirus

US-09-641-528-21757
 Query Match 80.0%; Score 16; DB 5; Length 8;
 Best Local Similarity 40.0%; Pred. No. 3e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;
 Qy 1 FXXXXW 5
 Db 4 FSRTW 8

RESULT 8
 US-09-641-528-22468
 Sequence 22468, Application US/09641528
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Chesnut, Robert
 APPLICANT: Celis, Esteban
 APPLICANT: Grey, Howard
 TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
 TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
 FILE REFERENCE: 2060_010001
 CURRENT APPLICATION NUMBER: US/09/641,528
 CURRENT FILING DATE: 2000-08-15
 PRIOR APPLICATION NUMBER: US 60/172,705
 PRIOR FILING DATE: 1999-12-10
 NUMBER OF SEQ ID NOS: 51504
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 22468
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide Derived from Human Papillomavirus

US-09-641-528-22468
 Query Match 80.0%; Score 16; DB 5; Length 8;
 Best Local Similarity 40.0%; Pred. No. 3e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;
 Qy 1 FXXXXW 5
 Db 4 FSRTW 8

RESULT 9
 US-09-641-528-22509
 Sequence 22509, Application US/09641528
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Chesnut, Robert
 APPLICANT: Celis, Esteban
 APPLICANT: Grey, Howard
 TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
 TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
 FILE REFERENCE: 2060_010001
 CURRENT APPLICATION NUMBER: US/09/641,528
 CURRENT FILING DATE: 2000-08-15
 PRIOR APPLICATION NUMBER: US 60/172,705
 PRIOR FILING DATE: 1999-12-10
 NUMBER OF SEQ ID NOS: 51504
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 22509
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide Derived from Human Papillomavirus

US-09-641-528-22509
 Query Match 80.0%; Score 16; DB 5; Length 8;
 Best Local Similarity 40.0%; Pred. No. 3e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;
 Qy 1 FXXXXW 5
 Db 4 FSRTW 8

RESULT 10
 US-09-641-528-31337
 Sequence 31337, Application US/09641528
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Chesnut, Robert
 APPLICANT: Celis, Esteban
 APPLICANT: Grey, Howard
 TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
 TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
 FILE REFERENCE: 2060_010001
 CURRENT APPLICATION NUMBER: US/09/641,528
 CURRENT FILING DATE: 2000-08-15
 PRIOR APPLICATION NUMBER: US 60/172,705
 PRIOR FILING DATE: 1999-12-10

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; NUMBER OF SEQ ID NOS: 51594
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 31337
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-31337

Query Match          80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 FXXXW 5
Db      2 FSRTW 6

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 31881
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-35881

Query Match          80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 FXXXW 5
Db      2 FSRTW 6

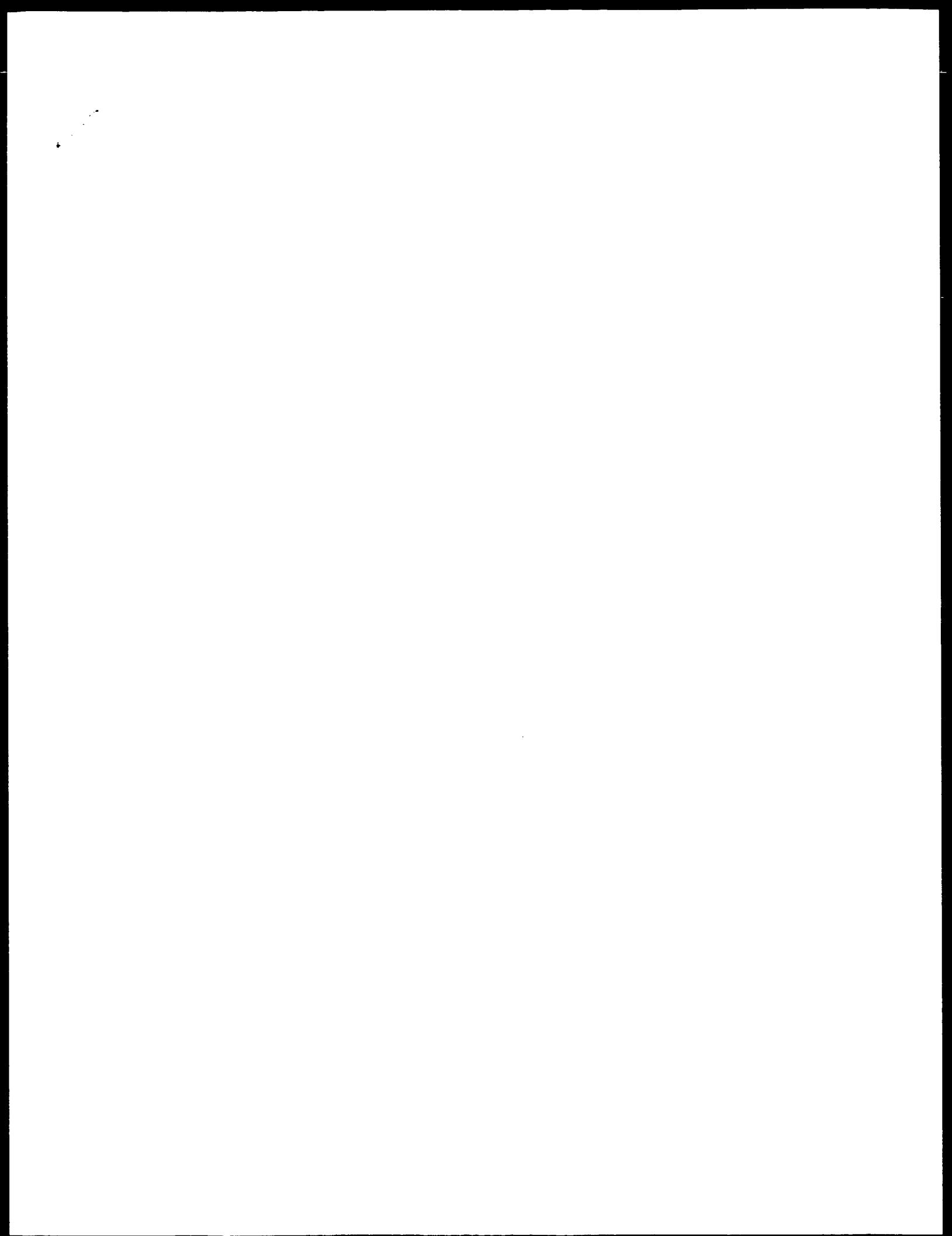
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; SEQ ID NO 41710
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
; US-09-641-528-41710
; QUERY Match Similarity 80.0%; Score 16; DB 5; Length 8;
; Best Local Similarity 40.0%; Pred. No. 3e+05;
; Matches 2; Conservative 0; Mismatches 3; Indels 0;
; Gaps 0;
; Qy 1 FXXW 5
; Db 2 FSRTW 6

RESULT 15
US-09-641-528-42699
Sequence 42699 Application US/09641528
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
FILE REFERENCE: 2050_010001
CURRENT APPLICATION NUMBER: US 09/641, 528
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51504
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42699
LENGTH: 8
TYPE: PRT
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-42699

Query Match Similarity 80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0;
Gaps 0;
Qy 1 FXXW 5
Db 2 FSRTW 6

Search completed: January 29, 2003, 14:21:05
Job time : 18 secs



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OM protein - protein search, using SW model
Run on: January 29, 2003, 14:16:08 ; Search time 14 Seconds
Perfect score: 10.508 Million cell updates/sec

Title: US-09-403-440a-4
Perfect score: 20
Sequence: FXXXW 5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Listing first 45 summaries
Issued Patents-AA:*

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2: /cgn2_6/ptodata/l/iaa/5b_COMB_pep: *
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4: /cgn2_6/ptodata/l/iaa/6b_COMB_pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	17	85.0	13 4	US-09-085-072-7
2	16	80.0	6 1	US-07-920-519-10
3	16	80.0	6 1	US-08-086-410-7
4	15	80.0	6 1	US-08-314-586-10
5	16	80.0	10 1	US-08-208-886C-87
6	16	80.0	10 1	US-08-704-744-89
7	16	80.0	10 1	US-08-469-557-68
8	16	80.0	10 2	US-08-290-793B-68
9	16	80.0	11 1	US-08-277-660A-16
10	16	80.0	11 1	US-08-277-660A-17
11	16	80.0	11 1	US-08-424-957-29
12	16	80.0	11 1	US-08-424-957-30
13	16	80.0	11 1	US-09-035-686-29
14	16	80.0	11 4	US-09-035-686-30
15	16	80.0	12 2	US-08-406-330-32
16	16	80.0	12 2	US-08-556-597-32
17	16	80.0	13 1	US-08-305-871A-23
18	16	80.0	13 1	US-08-912-560-11
19	16	80.0	13 4	US-08-788-822A-27
20	16	80.0	13 6	518541-25
21	16	80.0	15 1	US-08-218-025A-139
22	16	80.0	15 4	US-08-847-844A-32
23	16	80.0	15 5	PCT-US93-006699-1
24	16	80.0	16 4	US-09-330-914A-11
25	16	80.0	17 1	US-08-218-025A-115
26	16	80.0	17 2	US-08-746-283-7
27	16	80.0	17 2	US-08-746-257A-5

ALIGNMENTS

RESULT 1 US-09-085-072-7

; Sequence 7, Application US/09085072
; Patient No. 6265150
; GENERAL INFORMATION:
; APPLICANT: L. Terrappen et al.
; TITLE OF INVENTION: PHAGE ANTIBODIES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ParentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US09/085,072
; FILING DATE: 26 MAY - 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fejt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: 890-2 FWC/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3350
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-085-072-7

Query Match Score 85.0%; DB 4; Length 13;
Best Local Similarity 40.0%; Pred. No. 8.7e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5 |
Db 6 FASSW 10

RESULT 2

Sequence 10, Application US/07920519
; Patent No. 5,582,518
; GENERAL INFORMATION:
; APPLICANT: CAPOT, DANIEL
; APPLICANT: FERRARA, PASCUAL
; APPLICANT: GUILLEMOT, JEAN-CLAUDE
; APPLICANT: KACHAD, MOUARD
; APPLICANT: LEGOUX, RICHARD
; APPLICANT: LOISON, GERARD
; APPLICANT: LARRE, ELIZABETH
; APPLICANT: LUFPER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN, EXPRESSION VECTOR,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; COMPUTER TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,519
; FILING DATE: 10-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/659,408
; FILING DATE: 02-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; LENGTH: 6 amino acids
; REFERENCE/DOCKET NUMBER: 16781/276 BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEX: (703) 683-4109
; FAX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLogy: linear
; MOLECULE TYPE: peptide
; HYPOThETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: Hydrolysis product T23
; US-07-920-519-10
; Query Match 80.0%; Score 16; DB 1; Length 6;
; Best Local Similarity 40.0%; Pred. No. 1.9e+05;
; Matches 2; Conservative 0; Mismatches 3; Indels 0;
; Gaps 0;
; Qy 1 FXXXW 5
; Db 1 FDATW 5
; RESULT 3
; US-08-086-410-7
; Query Match 80.0%; Score 16; DB 1; Length 6;
; Best Local Similarity 40.0%; Pred. No. 1.9e+05;
; Matches 2; Conservative 0; Mismatches 3; Indels 0;
; Gaps 0;
; Qy 1 FXXXW 5
; Db 1 FDATW 5
; RESULT 4
; US-08-314-586-10
; Sequence 10, Application US/08314586
; Patent No. 5,541,098
; GENERAL INFORMATION:
; APPLICANT: CAPOT, DANIEL
; APPLICANT: FERRARA, PASCUAL
; APPLICANT: GUILLEMOT, JEAN-CLAUDE
; APPLICANT: KACHAD, MOUARD
; APPLICANT: LEGOUX, RICHARD
; APPLICANT: LOISON, GERARD
; APPLICANT: LARRE, ELIZABETH
; APPLICANT: LUFPER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; APPLICANT: LAURENT, PATRICK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; TITLE OF INVENTION: MICROORGANISMS AND TRANSFORMED CELLS
; APPLICANT: PESSEGUE, Bernard
; APPLICANT: SHIRE, David
; TITLE OF INVENTION: Artificial promoter for the expression
; TITLE OF INVENTION: of proteins in yeast
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; STREET: Road, PO Box 299
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; COMPUTER TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,410
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,083
; FILING DATE: 02-OCT-1991
; APPLICATION NUMBER: FR 89 17467
; FILING DATE: 29-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLogy: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: hydrolysis product T23
; US-08-086-410-7
; Query Match 80.0%; Score 16; DB 1; Length 6;
; Best Local Similarity 40.0%; Pred. No. 1.9e+05;
; Matches 2; Conservative 0; Mismatches 3; Indels 0;
; Gaps 0;
; Qy 1 FXXXW 5
; Db 1 FDATW 5
; RESULT 4
; US-08-314-586-10
; Sequence 10, Application US/08314586
; Patent No. 5,541,098
; GENERAL INFORMATION:
; APPLICANT: CAPOT, DANIEL
; APPLICANT: FERRARA, PASCUAL
; APPLICANT: GUILLEMOT, JEAN-CLAUDE
; APPLICANT: KACHAD, MOUARD
; APPLICANT: LEGOUX, RICHARD
; APPLICANT: LOISON, GERARD
; APPLICANT: LARRE, ELIZABETH
; APPLICANT: LUFPER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; APPLICANT: LAURENT, PATRICK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; TITLE OF INVENTION: MICROORGANISMS AND TRANSFORMED CELLS

NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/314,586
 FILING DATE: 28 SEP-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/659,408
 FILING DATE: 25-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REFERENCE/DOCKET NUMBER: 29,768
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO
 IMMEDIATE SOURCE:
 CLONE: Hydrolysis product T 23
 ; US-08-314-586-10

Query Match 80.0%; Score 16; DB 1; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.9e+05; Mismatches 0;
 Matches 2; Conservative 0; Indels 0; Gaps 0;
 QY 1 FXXW 5
 Db 1
 1 FDWTW 5

RESULT 5
 US 08-208-886C-87
 Sequence 87, Application US/08208886C
 ; Patient No. 559710
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalle, Barbara
 ; APPLICANT: Miller, Kenneth
 ; APPLICANT: Murgolo, Nicholas
 ; APPLICANT: Tindall, Stephen
 ; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
 ; NUMBER OF SEQUENCES: 90
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schering-Plough Corporation
 ; STREET: 2000 Galloping Hill Road
 ; CITY: Kenilworth
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07033-0530

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.5.3
 SOFTWARE: Microsoft Word 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/704,744
 FILING DATE: 06-SEPT-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/208886
 FILING DATE: 10-MAR-1994
 APPLICATION NUMBER: PCT/US95/024400
 FILING DATE: 08-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Foulke, Cynthia L.
 REFERENCE/DOCKET NUMBER: 32,364
 REFERENCE/DOCKET NUMBER: JBO429K
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 298-2987
 TELEFAX: (908) 298-5388
 INFORMATION FOR SEQ ID NO: 89:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids

TYPE: amino acid
 STRANDEDNESS: single
 US-08-704-744-89
 Query Match 80 0%; Score 16; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;
 Dr. 4 FSSYW 8

RESULT 7 US-08-469-557-68
 ; Sequence 68, Application US/08469557
 ; Patent No. 5770403
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalle, Barbara
 ; LE, Hung
 ; APPLICANT: Miller, Kenneth
 ; Miller, Kenneth
 ; APPLICANT: Murgolo, Nicholas
 ; Nguyen, Hanh
 ; APPLICANT: Tindall, Stephen
 ; Zavodny, Paul
 ; TITLE OF INVENTION: Cloning and Expression of
 ; Humanized Monoclonal Antibodies
 ; TITLE OF INVENTION: Against Human Interleukin-4
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schering-Plough Corporation
 ; STREET: 2000 Galloping Hill Road
 ; CITY: Kenilworth
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07033-0330
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 6.0.5
 ; SOFTWARE: Microsoft Word 5.1A
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/469, 557
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/290, 793
 ; FILING DATE: August 16, 1994
 ; APPLICATION NUMBER: PCT/US93/01301
 ; FILING DATE: 19-FEB-1992
 ; APPLICATION NUMBER: US 07/841, 659
 ; FILING DATE: 19-FEB-1992
 ; APPLICATION NUMBER: US 07/782, 784
 ; FILING DATE: 24-OCT-1991
 ; APPLICATION NUMBER: US 07/499, 327
 ; FILING DATE: 21-MAY-1990
 ; APPLICATION NUMBER: PCT/US88/03631
 ; FILING DATE: 21-OCT-1988
 ; APPLICATION NUMBER: US 06/843, 958
 ; FILING DATE: 14-FEB-1991
 ; APPLICATION NUMBER: US 07/113, 623
 ; FILING DATE: 26-OCT-1987
 ; APPLICATION NUMBER: US 06/881, 553
 ; FILING DATE: 03-JUL-1986
 ; APPLICATION NUMBER: US 06/843, 958
 ; FILING DATE: 25-MAR-1986
 ; APPLICATION NUMBER: US 06/799, 668
 ; FILING DATE: 19-NOV-1985
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Foulke, Cynthia L.
 ; REGISTRATION NUMBER: 32,364
 ; REFERENCE/DOCKET NUMBER: 2409K7

RESULT 8 US-08-290-793B-68
 ; Sequence 68, Application US/08290793B
 ; Patent No. 5863537
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalle, Barbara
 ; LE, Hung
 ; APPLICANT: Miller, Kenneth
 ; Miller, Kenneth
 ; APPLICANT: Murgolo, Nicholas
 ; Nguyen, Hanh
 ; APPLICANT: Tindall, Stephen
 ; Zavodny, Paul
 ; TITLE OF INVENTION: Cloning and Expression of
 ; Humanized Monoclonal Antibodies
 ; TITLE OF INVENTION: Against Human Interleukin-4
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schering-Plough Corporation
 ; STREET: 2000 Galloping Hill Road
 ; CITY: Kenilworth
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07033-0330
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 6.0.5
 ; SOFTWARE: Microsoft Word 5.1A
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/290, 793B
 ; FILING DATE: August 16, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/01301
 ; FILING DATE: 19-FEB-1992
 ; APPLICATION NUMBER: US 07/841, 659
 ; FILING DATE: 19-FEB-1992
 ; APPLICATION NUMBER: US 07/782, 784
 ; FILING DATE: 24-OCT-1991
 ; APPLICATION NUMBER: US 07/499, 327
 ; FILING DATE: 21-MAY-1990
 ; APPLICATION NUMBER: PCT/US88/03631
 ; FILING DATE: 21-OCT-1988
 ; APPLICATION NUMBER: US 07/655, 966
 ; FILING DATE: 14-FEB-1991
 ; APPLICATION NUMBER: US 07/113, 623
 ; FILING DATE: 26-OCT-1987
 ; APPLICATION NUMBER: US 06/881, 553
 ; FILING DATE: 03-JUL-1986
 ; APPLICATION NUMBER: US 06/843, 958
 ; FILING DATE: 25-MAR-1986
 ; APPLICATION NUMBER: US 06/799, 668
 ; FILING DATE: 19-NOV-1985
 ; ATTORNEY/AGENT INFORMATION:

NAME: Foulke, Cynthia L.
 REGISTRATION NUMBER: 32,364
 REFERENCE/DOCKET NUMBER: 2409K7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-298-2887
 TELEFAX: 908-298-5388
 INFORMATION FOR SEQ ID NO: 68:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-290-793B-68

Query Match 80.0%; Score 16; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.2e+03; 3;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;

QY 1 FXXXW 5
 |
 Db 4 FSSYW 8

RESULT 9
 US-08-277-660A-16
 Sequence 16, Application US/08277660A
 Patent No. 5702908
 GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.
 APPLICANT: Lane, David P.
 APPLICANT: Flehr, Hohbach, Test, Albritton & Herbert
 TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
 NUMBER OF SEQUENCES: 27
 TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/277,660A
 FILING DATE: 20-JUL-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-60244/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-277-660A-17

Query Match 80.0%; Score 16; DB 1; Length 11;
 Best Local Similarity 40.0%; Pred. No. 1.2e+03; 3;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;

QY 1 FXXXW 5
 |
 Db 5 FSDAW 9

RESULT 11
 US-08-424-957-29
 Sequence 29, Application US/08424957
 Patent No. 5770377
 GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.
 APPLICANT: Lane, David P.
 APPLICANT: Flehr, Hohbach, Test, Albritton & Herbert
 TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 80.0%; Score 16; DB 1; Length 11;
 Best Local Similarity 40.0%; Pred. No. 1.2e+03; 3;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;

QY 1 FXXXW 5
 |
 Db 5 FSALW 9

SOFTWARE: Patentin Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,957
 FILING DATE: 19-APR-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/277,660
 FILING DATE: 20-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 08-424-957-29

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RESULT 13
US-09-035-686-29
; Sequence 29, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Picklesley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF INVENTIONS: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fiehr, Rohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035, 686
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424, 957
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24, 190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-29

Query Match          80.0%; Score 16; DB 4; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.2e+03; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Topology: unknown
US-09-035-686-30
; Sequence 30, Application US/09035686

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Patent No. 6153391
GENERAL INFORMATION:

APPLICANT: Picklesley, Steven M.

APPLICANT: Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDM2 and p53

TITLE OF INVENTION: Protein and Therapeutic Application Thereof

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: US/08/406,330

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Timian, Susan J.

REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 20884/1100

TELECOMMUNICATION INFORMATION:

TELEPHONE: (716) 263-1636

TELEFAX: (716) 263-1600

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-406-330-32

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Matches	40.0%;	Conservative	0;	Mismatches
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Db	3 FSSW 7			

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,330
FILING DATE: US/08/406,330
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

Search completed: January 29, 2003, 14:18:21
Job time : 15 secs

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/424,957

FILING DATE: 19-APR-1995

APPLICATION NUMBER: US 08/277,660

FILING DATE: 20-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-61228/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 338-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

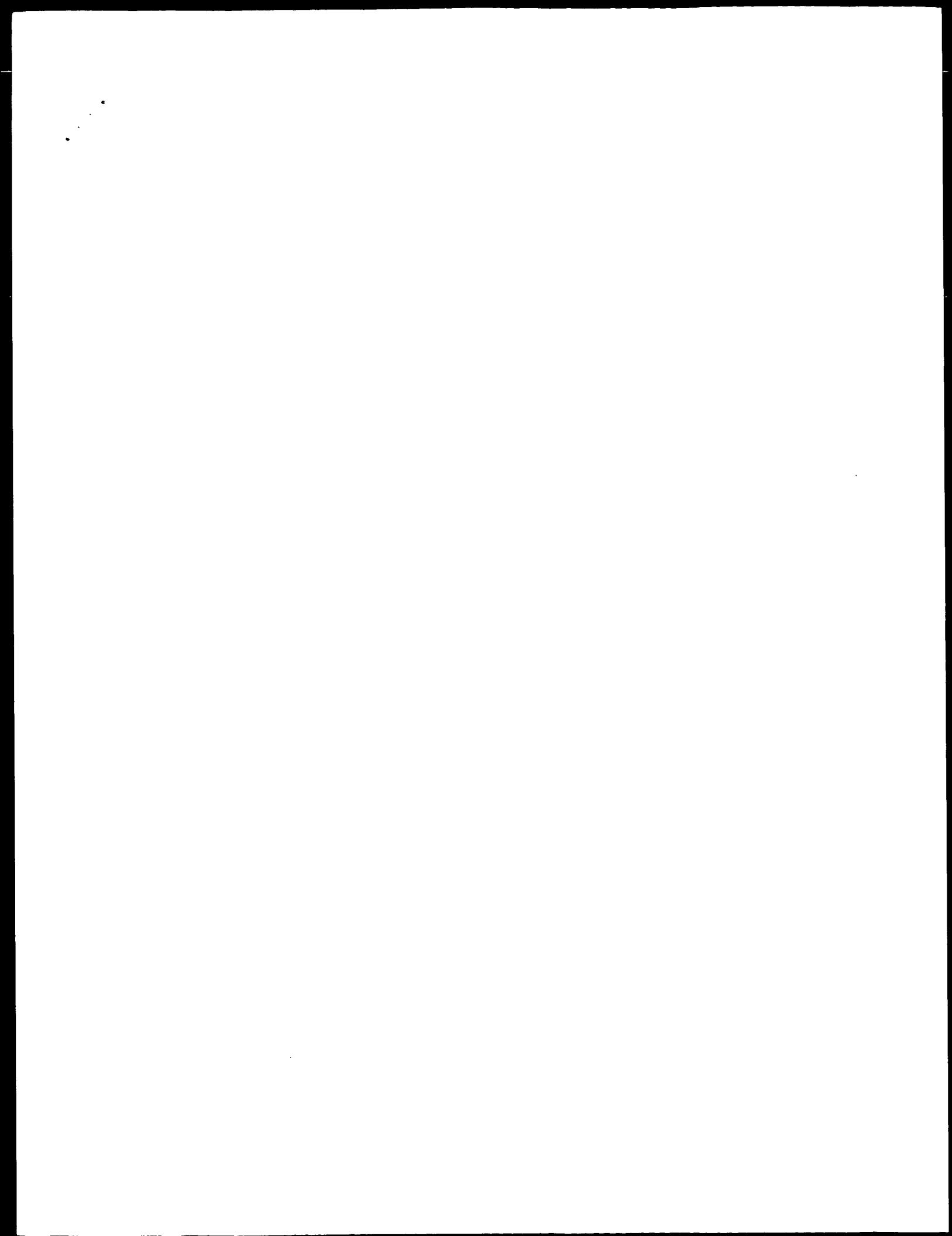
US-08-406-330-32

Query Match Score 80.0%; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0;
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QY 1 FXXXW 5
DB 3 FSSW 7

US-08-406-330-32

Sequence 32, Application US/08/06330
Patent No. 5817748
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MINIMOTOPES AND ANTI-MINIMOTOPES OF HUMAN PLATELET GLYCOPROTEIN 1b/IX
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible



copyright (c) 1993 - 2003 Compugen Ltd.	Gencore version 5.1.3				
OM protein - protein search, using SW model					
Run on:	January 29, 2003, 14:21:09 ; Search time 14 Seconds				
Perfect score:	34.334 Million cell updates/sec				
Sequence:	1 FXXXW 5				
Scoring table:	BLOSUM62				
Searched:	Gapext 0.5				
Total number of hits satisfying chosen parameters:	283224 seqs, 96134422 residues				
Minimum DB seq length:	5				
Maximum DB seq length:	5				
Post-processing:	Minimum Match 0%; Maximum Match 100%				
Database :	Listing first 45 summaries				
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1: pir1;*					
2: pir2;*					
3: pir3;*					
4: pir4;*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	120				
Searched:					
Length:					
Alignments:					
Summary:					
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3	11	55.0	2	2	JH0253
4	11	55.0	5	2	G37196
5	11	55.0	5	2	PT0281
6	11	55.0	5	2	PT0308
7	11	55.0	5	2	PT0729
8	11	55.0	5	2	PT0580
9	6	30.0	5	2	A44956
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12	6	30.0	5	2	B45525
13	6	30.0	5	2	AK4692
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15	6	30.0	5	2	A61445
16	6	30.0	5	2	JS0319
17	6	30.0	5	2	B61168
18	6	30.0	5	2	PT0278
19	6	30.0	5	2	PT0644
20	6	30.0	5	4	A55728
21	3	15.0	5	1	HOROHA
22	3	15.0	5	2	B37325
23	3	15.0	5	2	139964
24	3	15.0	5	2	139966
25	3	15.0	5	2	I39965
26	3	15.0	5	2	144469
27	3	15.0	5	2	E60274
28	3	15.0	5	2	F22565
29	3	15.0	5	2	P00009

RESULT 3
JH0253
gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Accession: JH0253
R;Iesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Bichem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
A;Accession: JH0253
A;Molecule type: protein
A;Residues: 1-5 <UES>
A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric junction of the circular muscle of the gastro-intestinal junction.

Query Match	Best Local Similarity	Score	DB	Length	Pred. No.	Mismatches	Indels	Gaps	0;
QY	5 W 5	55.0%	DB 2;	Length 5;		0;			
Db	3 W 3								

RESULT 4
G3196
bradykinin-potentiating peptide 7 - island jiraraca
C;Species: Bothrops insularis (island jararaca)
C;Accession: G3196
C;Accession: G3196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis (island jararaca).
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: G3196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CINS>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental

Query Match	Best Local Similarity	Score	DB	Length	Pred. No.	Mismatches	Indels	Gaps	0;
QY	5 W 5	55.0%	DB 2;	Length 5;		0;			
Db	2 W 2								

RESULT 5
PT0281
Ig heavy chain CRD3 region (clone 4-9IC) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0281
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0281
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match	Best Local Similarity	Score	DB	Length	Pred. No.	Mismatches	Indels	Gaps	0;
QY	5 W 5	55.0%	DB 2;	Length 5;		0;			
Db	3 W 3								

RESULT 6
PT0308
Ig heavy chain CRD3 region (clone 6-8B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0308
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0308
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match	Best Local Similarity	Score	DB	Length	Pred. No.	Mismatches	Indels	Gaps	0;
QY	5 W 5	55.0%	DB 2;	Length 5;		0;			
Db	2 W 2								

RESULT 7
PT0729
T-cell receptor beta chain V-D-J region (120-1U) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: PT0729
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601; PMID:171558
A;Accession: PT0640
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <PEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A;Accession: PT0640
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <PE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
A;Accession: PT0729
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <PE3>
A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C;Keywords: T-cell receptor

Query Match	Best Local Similarity	Score	DB	Length	Pred. No.	Mismatches	Indels	Gaps	0;
QY	5 W 5	55.0%	DB 2;	Length 5;		0;			
Db	5 W 5								

RESULT 8
PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0580

R;Reehey, A.J.
J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <PFE>

A;Experimental source: day 19 fetal thymus, strain BALB/C

C;Keywords: T-cell receptor

Query Match 55.0%; Score 11; DB 2; Length 5;
best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5
Db 4 W 4

RESULT 9

A44955 alkenal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - *Vibrio harveyi* (fragment)

C;Species: *Vibrio harveyi*
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000

R;Paquette, O.; Tu, S.C.
Photochem. Photobiol. 50, 817-825, 1989

A;Title: Chemical modification and characterization of the alpha cysteine 106 at the vib

A;Reference number: A44955; MUID:90175700; PMID:262493

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <PAQ>

C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 30.0%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
Db 1 F 1

RESULT 10

S70615 endo-1,4-beta-xylanase (EC 3.2.1.8) - *Streptomyces* sp. (*Chainia* sp. NCL 82.5.1) (fragment)

N;Alternate names: xylanase
C;Species: *Streptomyces* sp.

A;Variety: *Chainia* sp. NCL 82.5.1

C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999

C;Accession: S70615

R;Rao, M.; Khadikar, S.; Bandivadekar, K.R.; Deshpande, V.

Biochem. J 316, 771-75, 1996

A;Title: Structural environment of an essential cysteine residue of xylanase from *Chainia*

A;Reference number: S70615; MUID:96265041; PMID:8670151

A;Molecule type: protein

A;Residues: 1-5 <RAO>

A;Experimental source: *Chainia* sp. strain NCL 82.5.1

A;Note: the source is designated as *Chainia* sp.

C;Function:

A;Description: endohydrolyzation of beta-1,4-xylidosic linkages in xylans

C;Keywords: glycosidase; hydrolase

Query Match 30.0%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
Db 1 F 1

Db 3 F 3

RESULT 11

P50324 ribulose-bisphosphate carboxylase activase III - rice (strain Nihonpare) (fragment)

C;Species: *Oryza sativa* (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998

C;Accession: PS0324

R;Tsugita, A.

submitted to JIPID, April 1993

A;Reference number: PS0206

A;Accession: PS0324

A;Molecule type: protein

A;Residues: 1-5 <TSU>

A;Experimental source: leaf, chlorophyll

Query Match 30.0%; Score 6; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
Db 1 F 1

RESULT 12

B45525 actin I - malaria parasite (*Plasmodium falciparum*) (fragments)

C;Species: *Plasmodium falciparum*

C;Accession: B45525

R;Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoen

Mol. Biochem. Parasitol. 35, 167-176, 1989

A;Title: Stage-specific expression and genomic organization of the actin genes of the

A;Reference number: B45525; MUID:8364996; PMID:2671721

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-5 <WES>

A;Cross-references: GB:J03988

A;Note: the authors translated the codon GAA for residue 3 as GLY

C;Comment: The actin 1 gene contains no introns.

Query Match 30.0%; Score 6; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
Db 5 F 5

RESULT 13

A44692 fulicin - giant African snail

C;Species: *Achatina fulica* (giant African snail)

C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997

C;Accession: A44692

R;Ohta, N.; Kubota, I.; Takao, T.; Shionishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.;

Biochem. Biophys. Res. Commun. 178, 486-493, 1991

A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated fro

A;Reference number: A44692; MUID:91315471; PMID:1859408

A;Accession: A44692

A;Molecule type: protein

A;Residues: 1-5 <OH>

C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide

F;2/Modified site: D-asparagine (asn) #status experimental

F;5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 30.0%; Score 6; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
Db 1 F 1

QY	1	F	1
Db	1	F	1

RESULT 14

B61445

Leu-enkephalin - blue mussel

C;Species: Mytilus edulis (blue mussel)

C;Date: 07-oct-1994 #sequence_revision 07-oct-1994 #text_change 21-Jan-2000

C;Accession: B61445

R.;Læung, M.K.; Stefano, G.B.

PROC: Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis

A;Reference number: A61445; MUID:84144823; PMID:653690

A;Accession: B61445

A;Molecule type: protein

A;Residues: 1-5 <LEU>

A;Experimental source: pedal ganglia

C;Keywords: neuropeptide; opioid peptide

Query Match 30.0%; Score 6; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0;

Matches 1; Conservative 0; Gaps 0;

QY 1 F 1

Db 4 F 4

RESULT 15

A61445

Met-enkephalin - blue mussel

C;Species: Mytilus edulis (blue mussel)

C;Date: 07-oct-1994 #sequence_revision 07-oct-1994 #text_change 21-Jan-2000

C;Accession: A61445

R.;Læung, M.K.; Stefano, G.B.

PROC: Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis

A;Reference number: A61445; MUID:84144823; PMID:653690

A;Accession: A61445

A;Molecule type: protein

A;Residues: 1-5 <LEU>

A;Experimental source: pedal ganglia

C;Keywords: neuropeptide; opioid peptide

Query Match 30.0%; Score 6; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0;

Matches 1; Conservative 0; Gaps 0;

QY 1 F 1

Db 4 F 4

Search completed: January 29, 2003, 14:23:17
Job time : 14 secs

DE Carcinustatin 14.
 OS *Carcinus maenas* (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacei;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Ploctyemata;
 OC Brachyura; Eubrachyura; Portunoidea; Portunidae; *Carcinus*.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE="cerebral ganglion, and "Thoracic ganglion;"
 RX MEDLINE=98121193; PubMed=9401295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.,
 RT "Isolation and identification of multiple neuropeptides of the
 allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 205:727-734 (1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 5 AA; 556 MW; 672879D5AB300000 CRC64;
 SEQUENCE 5 AA; 556 MW; 672879D5AB300000 CRC64;
 (Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 F 1
 Db 3 F 3

RESULT 4
 E103_LITRU STANDARD: PRT; 5 AA.
 ID E103_LITRU
 AC PB2099;
 DT 15-JUN-2002 (Rel. 41; Created)
 DT 15-JUN-2002 (Rel. 41; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Electrin 3.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Peleodryadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria rubella.,"
 RL Aust. J. Chem. 52:639-645 (1999).
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5 AA; 616 MW; 61F2D1R059A00000 CRC64;
 SEQUENCE 5 AA; 616 MW; 61F2D1R059A00000 CRC64;
 (Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 F 1
 Db 1 F 1

RESULT 5
 E104_LITRU STANDARD: PRT; 5 AA.
 ID E104_LITRU
 AC PB2100;
 DT 15-JUN-2002 (Rel. 41; Created)
 DT 15-JUN-2002 (Rel. 41; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Electrin 4.

Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 F 1
 Db 1 F 1

RESULT 6
 FARP_ARTTR STANDARD: PRT; 5 AA.
 ID FARP_ARTTR
 AC P41833;
 DT 01-NOV-1995 (Rel. 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 01-NOV-1995 (Rel. 32; Last annotation update)
 DE FMRFamide-like peptide FMRF-amide.
 OS Articopisthia triangulata.
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
 OC Terricola; Geophilidae; Arthurendyus.
 OX NCBI_TaxID=132421;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC MEDLINE=94211927; PubMed=7909164;
 RA Mauli A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
 RT "RYIRFamide: a turbellarian FMRFamide-related peptide (PaRP)." ;
 RL Regul. Pept. 50:37-43 (1994).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC -!- FAMILY: Articopisthia triangulata.
 KW Neuropeptide; Amidation.
 FT MOD_RES 5 AA; 754 MW; 69d4004B4460000 CRC64;
 SEQUENCE 5 AA; 754 MW; 69d4004B4460000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 F 1
 Db 5 F 5

RESULT 7
 PAP2_PARMA STANDARD: PRT; 5 AA.
 ID PAP2_PARMA
 AC P81864;
 DT 30-MAY-2000 (Rel. 39; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Pardaxin II (PXXII) (Fragment).
 OS Pardachirus marmoratus (Red sea moses sole).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Buteostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
 OC Soleoidei; Soleidae; Pardachirini.

OX NCBI_TaxID=31087;
RN [1] DE 15-JUN-2002 (Rel. 41, Last annotation update)
RP OS Rubellidin 2,1.
RC TISSUE=Skin secretion;
RT OC Litoria rubella (Desert tree frog).
RX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
RT OC Pelodryadinae; Litoria.
RN OC NCBI_TaxID=104895;
RP TISSUE=Skin secretion;
RT RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
CC TYler M.J., Wallace J.C.;
PROPERTIES FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5
SEQUENCE 5 AA: 614 MW: 7769C9C8100000 CRC64;
Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 2 F 2

RESULT 8
RE11_LITRU STANDARD; PRT; 5 AA.

ID RE11_LITRU STANDARD; PRT; 5 AA.
AC P82070;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Rubellidin 1,1.
OS Litoria rubella (desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodryadinae; Litoria.
NCBI_TaxID=104895;
RN [1] SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RT Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog of evolutionary trends of amphibians.",
RT Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=593; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA: 598 MW: 6DD9C9CAB2A0000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
RE21_LITRU STANDARD; PRT; 5 AA.

QY 1 F 1
Db 3 F 3

RESULT 10
RE31_LITRU STANDARD; PRT; 5 AA.

ID RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Rubellidin 3,1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodryadinae; Litoria.
NCBI_TaxID=104895;
RN [1] SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RT Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog of evolutionary trends of amphibians.",
RT Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 5 5 AMIDATION.
SEQUENCE 5 AA: 656 MW: 71A9C9CB10300000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
RE32_LITRU

QY 1 F 1
Db 3 F 3

ID RE32-LITRU STANDARD; PRT; 5 AA.
 AC P82073;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 3.2.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=104695;
 RN [1]
 RP SEQUENCE:
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from *Litoria*
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9c862A00000 CRC64;
 Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 F 1
 Db 3 F 3

RESULT 12
 SUGA_ACHDO STANDARD; PRT; 5 AA.
 ID SUGA_ACHDO STANDARD; PRT; 5 AA.
 AC P11931;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Suboesophageal ganglion penicapeptide.
 OS Acheta domesticus (House cricket).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;
 OC Gryllidae; Gylliniae; Acheta.
 RN [1]
 RP SEQUENCE.
 RA Wicker C.;
 RT "Isolation and structure of a peptide isolated from the
 suboesophageal ganglion of *Acheta domesticus* (orthoptera)." ;
 RL Comp. Biolog. Physiol. 88C:185-187(1987).
 CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL
 CC GANGLIA.
 DR PIR; JS0319; JS0319;
 RA SEQUENCE 5 AA; 476 MW; 69D76DDDD000000 CRC64;

(Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 F 1
 Db 5 F 5

RESULT 13
 TPIS_CANFA STANDARD; PRT; 5 AA.
 ID TPIS_CANFA STANDARD; PRT; 5 AA.
 AC P5474;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 F 1

ID DT 15-JUL-1998 (Rel. 36, Last annotation update)
 AC DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
 GN TPIL
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RA MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glyceroen
 phosphate.
 CC -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
 DR HSC-2DPAGE; P54714; DOG.
 DR InterPro; IPR00652; Triphos_ismre.
 DR PROSITE; PS00171; TIM; PARTIAL.
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
 KW Pentose shunt.
 FT NON_TER 5 5 5 MW; 64444862C9A00000 CRC64;
 FT NON_TER 1 1 1 MW; 550 MW;
 SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;
 Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 F 1
 Db 1 F 1

RESULT 14
 UG22_MAIZE STANDARD; PRT; 5 AA.
 ID UG22_MAIZE STANDARD; PRT; 5 AA.
 AC P80628;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Perrinlet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:937-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.1. ITS MW IS: 30.4 kDa.
 DR Maize 2DPAGE; P80628; COLEOPTILE.
 DR Maizedb; 123954; -.
 FT NON_TER 1 1 1 MW; 30.4 kDa;
 FT NON_TER 5 5 5 MW; 654 MW; 72CB19C9C0300000 CRC64;
 SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

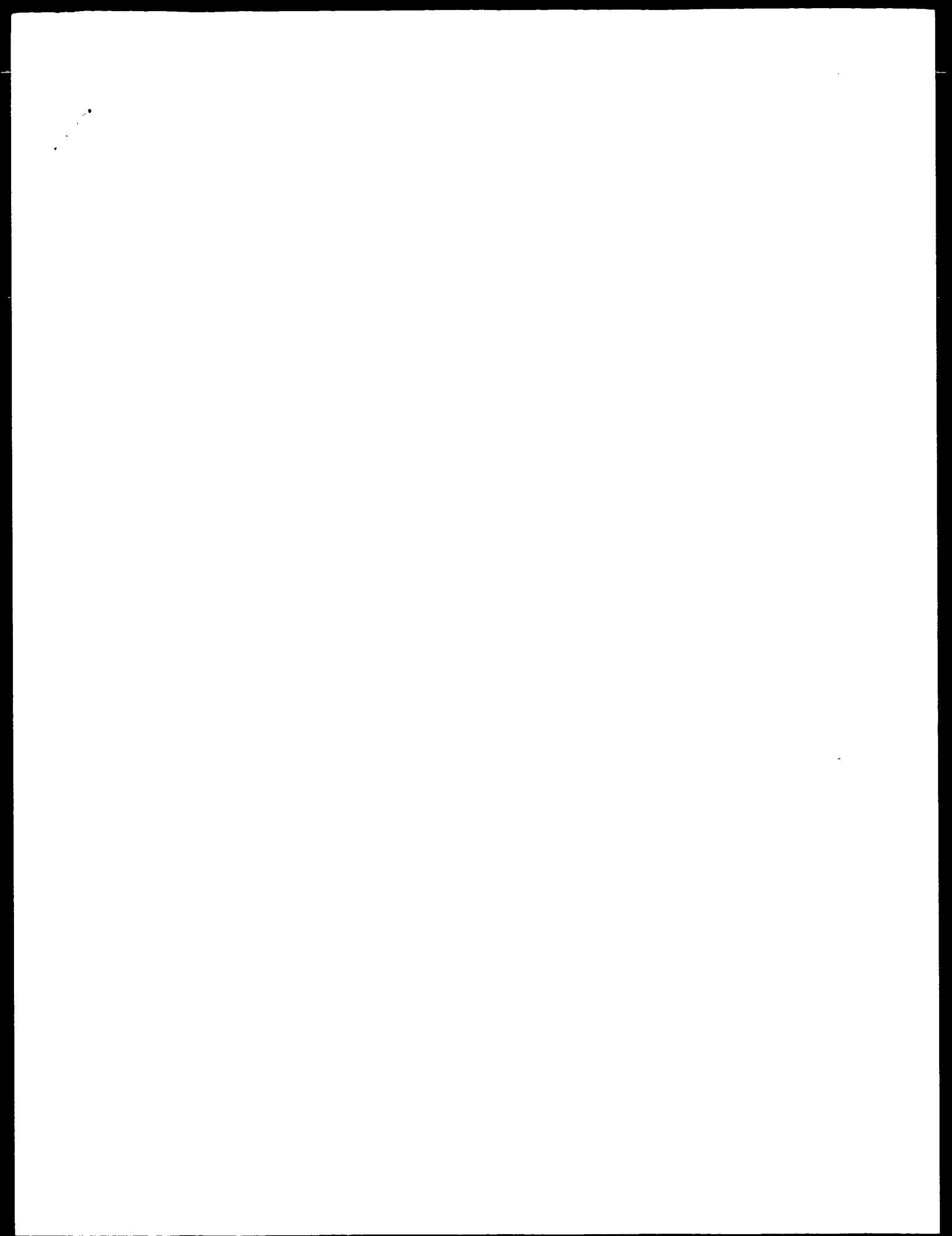
Query Match 30.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 F 2

RESULT 15

PRCT_PERAM	STANDARD;	PRT;	5 AA.
ID P01373;			
DT 21-JUL-1986 (Rel. 01, Created)			
DT 21-JUL-1986 (Rel. 01, last sequence update)			
DT 01-FEB-1995 (Rel. 31, last annotation update)			
DE proctolin.			
OC Periplaneta americana (American cockroach),			
OS Limulus polyphemus (Atlantic horseshoe crab), and			
OS Carcinus maenas (Common shore crab) (Green crab).			
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;			
OC Blattoidea; Blattidae; Periplaneta.			
OX NCBI-TaxID=6978, 6650, 6759;			
RN [1]			
RP SEQUENCE.			
RC SPECIES="P.americana";			
RX MEDLINE=6074708; PubMed=576;			
RA Starratt A.N., Brown B.E.;			
RT "Structure of the Pentapeptide proctolin, a proposed neurotransmitter in insects.,"			
RL Life Sci. 17:1253-1256(1975).			
RN [2]			
RP BIOLOGICAL SOURCE.			
RC SPECIES="P.americana";			
RX MEDLINE=81225665; PubMed=6113690;			
RA O'Shea M., Adams M.E.;			
RT "Pentapeptide (proctolin) associated with an identified neuron.,"			
RL Science 213:567-569(1981).			
RN [3]			
RP SEQUENCE.			
RC SPECIES="L.polyphemus";			
RX MEDLINE=60287800; PubMed=2356151;			
RA Groome J.R., Tillingshast E.K., Townley M.A., Vetrov A.;			
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,			
RA Shabanowitz J.;			
RT "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus.,"			
RL Peptides 11:205-211(1990).			
RN [4]			
RP SEQUENCE.			
RC SPECIES="C.maenas";			
RX MEDLINE=66232789; PubMed=28722661;			
RA Stangler J., Dirksen R., Keller R.;			
RT "Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, carcinus maenas.,"			
RL Peptides 7:67-72(1986).			
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,			
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS			
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN			
CC THE CRAB PERICARDIAL ORGANS.			
DR PIR: A01644; HOROHA.			
DR PIR: A60411; A60411.			
KW Neuropeptide.			
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC54;			
Query Match 15.0%; Score 3; DB 1; Length 5;			
Best Local Similarity 0.0%; Pred. No. 1,1e+05;			
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY 1 F 1			
Db 2 Y 2			

Search completed: January 29, 2003, 14:22:21
Job time : 12 secs



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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:20:44 ; Search time 28 Seconds

(without alignments)
36.794 Million cell updates/secTitle: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen parameters: 3
Minimum DB seq length: 5
Maximum DB seq length: 5Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SPTREMBL_21:*
- 2: sp_archea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mammal:*
- 8: sp_mhc:*
- 9: sp_organelle:*
- 10: sp_phage:*
- 11: sp_plant:*
- 12: sp_rabbit:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	6	30.0	5	13 P83308	P83308 gallus galli
2	0	0.0	5	2 P83073	P83073 bacillus ce
3	0	0.0	5	10 Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1

ID	P83308	PRELIMINARY;	PRT;	5 AA.
AC	P83308;			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	ENRfamide-like neuropeptide (LIPRF-amide).			

OS Gallus gallus (Chicken).
OC Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=BRAIN;
RX PubMed=6137771;
RA Dockrey G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by antibodies to FMRFamide.";
RL Nature 305:328-330(1983).
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA: 69D4073767400000 CRC64;
Query Match 30.0%; Score 6; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 5 F 5

RESULT 2

ID	P83073	PRELIMINARY;	PRT;	5 AA.
AC	P83073;			
DT	01-OCT-2001 (TREMBLrel. 18, Created)			
DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)			
DE	88 kDa protein (Fragment).			
OS	Bacillus cereus			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;			
CC	Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1396;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=NCIMB 11796;			
RA	Browne N., Dowds B.C.A.;			
RL	Submitted (JUL-2001) to the SWISS-PROT data bank.			
FT	NON_TER 5			
SEQUENCE	5 AA: 623 MW: 6801AAA336F00000 CRC64;			
QY	Query Match 0.0%; Score 0; DB 2; Length 5; Best Local Similarity 0.0%; Pred. No. 6.7e+05; Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Db	1 M 1			

RESULT 3

ID	Q99007	PRELIMINARY;	PRT;	5 AA.
AC	Q99007;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
DE	Alpha-amylase (EC 3.2.1.1) (Fragment).			
GN	AMY1			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
CC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;			
OX	Triticaceae; Hordeum.			
NCBI_TaxID=4513;	[1]			
RN	SEQUENCE FROM N.A.			

RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V.; Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers." Plant Mol. Biol. 16:713-721(1991).
RL -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
CC -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
DR EMBL; X54643; CAA38455.1; -;
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON_TER 5
SEQUENCE 5 AA: 600 MW; 61E3344DDGF00000 CRC64;

Query Match 0 0%; Score 0; DB 10; Length 5;
Best Local Similarity 0 0%; Pred. No. 6.7e-05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 F 1
Db 1 M 1

Search completed: January 29, 2003, 14:22:55
Job time : 28 secs

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SUMMARIES

PN WO9634012-A1.
 XX
 PD 31-OCT-1996.
 XX
 PF 25-APR-1996; 96WO-JP01140.
 XX
 PR 09-MAY-1995; 95JP-0110933.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Furuya S, Kato K, Kitada C;
 XX
 DR WPI; 1996-497569/49.
 XX
 PT Cyclic penta:peptide(s), some new, as LH-RH receptor antagonists - used to treat or prevent sex hormone dependent disorders, e.g. cancer, also for control of pregnancy and menstruation and to improve meat quality in animals
 XX
 PS Example 40-41; Page 170; 198pp; English.
 XX
 CC This Peptide represents a cyclic peptide which is included in the luteinising hormone releasing hormone (LH-RH) receptor antagonist composition of the invention. Peptides such as this are used to prevent or treat sex hormone dependent disorders in human or veterinary medicine, esp. cancers (of the prostate, uterus, breast or pituitary), prostatomegaly, endometriosis, hysteroymoma or precocious puberty, but also amenorrhoea, premenstrual syndrome, multilocular ovarian syndrome, comedo, etc.; also to control pregnancy (contraception for men or women, also to induce ovulation) and the menstrual cycle. They are also used to control oestrus in animals, to improve meat quality and control growth, and to promote spawning in fish. They may also inhibit the transient increase in testosterone blood levels caused by admin. of superagonists such as leuprorelin acetate.
 XX
 Sequence 5 AA:
 Query Match 75.0%; Score 15; DB 17; Length 5;
 Best Local Similarity 60.0%; Pred. No. 7.7e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 QY 1 FXXXW 5
 SQ | | |
 Db 1 FRXAW 5
 DE
 RESULT 2
 AAW17812 standard; peptide; 5 AA.
 AC AAW17812;
 XX
 DT 07-JUL-1997 (first entry)
 XX
 DE Cyclic pentapeptide #28 used in LH-RH receptor antagonist.
 XX
 KW Luteinising hormone releasing hormone receptor; LH-RH; antagonist; sex-hormone; human; veterinary medicine; cancer; prostate; uterus; breast; pituitary; prostatomegaly; endometriosis; hysteroymoma; precocious puberty; amenorrhoea; premenstrual syndrome; cyclic; multilocular ovarian syndrome; comedo; pregnancy; contraception; ovulation; menstrual cycle; oestrus; meat quality; growth; spawning; fish; testostosterone; superagonist; leuprorelin acetate.
 XX
 Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Joined via a peptide linkage to Trp5"
 FT Modified-site 2
 FT /note= "N-Toluenesulphonylarginine, D-form residue"
 FT Modified-site 3
 FT /label= OTHER
 FT /note= "Parafluorophenylalanine"
 XX
 PN WO9634012-A1.
 FT Misc-difference 4 /note= "D-form residue"
 FT
 FT Modified-site 5 /note= "Joined via a peptide linkage to Phe1"
 XX
 OS Synthetic.
 XX
 PR 09-MAY-1995; 95JP-0110933.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Furuya S, Kato K, Kitada C;
 XX
 DR WPI; 1996-497569/49.
 XX
 PT Cyclic penta:peptide(s), some new, as LH-RH receptor antagonists - used to treat or prevent sex hormone dependent disorders, e.g. cancer, also for control of pregnancy and menstruation and to improve meat quality in animals
 XX
 PS Example 50; Page 176; 198pp; English.
 XX
 CC This Peptide represents a cyclic peptide which is included in the luteinising hormone releasing hormone (LH-RH) receptor antagonist composition of the invention. Peptides such as this are used to prevent or treat sex-hormone dependent disorders in human or veterinary medicine, esp. cancers (of the prostate, uterus, breast or pituitary), prostatomegaly, endometriosis, hysteroymoma or precocious puberty, but also amenorrhoea, premenstrual syndrome, multilocular ovarian syndrome, comedo, etc.; also to control pregnancy (contraception for men or women, also to induce ovulation) and the menstrual cycle. They are also used to control oestrus in animals, to improve meat quality and control growth, and to promote spawning in fish. They may also inhibit the transient increase in testosterone blood levels caused by admin. of superagonists such as leuprorelin acetate.
 XX
 Sequence 5 AA:
 Query Match 75.0%; Score 15; DB 17; Length 5;
 Best Local Similarity 60.0%; Pred. No. 7.7e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 QY 1 FXXXW 5
 SQ | | |
 Db 1 FRXAW 5
 DE
 RESULT 3
 AAW17806
 ID AAW17806 standard; peptide; 5 AA.
 AC AAW17806;
 XX
 DT 07-JUL-1997 (First entry)
 XX
 DE Cyclic pentapeptide #22 used in LH-RH receptor antagonist.
 XX
 KW Luteinising hormone releasing hormone receptor; LH-RH; antagonist; sex-hormone; human; veterinary medicine; cancer; prostate; uterus; breast; pituitary; prostatomegaly; endometriosis; hysteroymoma; precocious puberty; amenorrhoea; premenstrual syndrome; cyclic; multilocular ovarian syndrome; comedo; pregnancy; contraception; ovulation; menstrual cycle; oestrus; meat quality; growth; spawning; fish; testostosterone; superagonist; leuprorelin acetate.
 XX
 Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Joined via a peptide linkage to Trp5"
 FT Modified-site 2
 FT /note= "N-Toluenesulphonylarginine, D-form residue"
 FT Modified-site 3
 FT /label= OTHER
 FT /note= "Parafluorophenylalanine"
 XX
 FH Key Location/Qualifiers

FT	MOCRiled-site	1	/note= "joined via a peptide linkage to Trp5, opt.
FT			parachlorophenylalanine"
FT	MISC-difference	2	/note= "opt. N-(4-methoxy-2,3,6-trimethylbenzene-sulphonylarginine, opt. D-form residue"
FT			
FT	Modified-site	3	/note= "opt. Parachlorophenylalanine"
FT			
FT	Misc-difference	4	/note= "D-form residue"
FT			
FT	Modified-site	5	/note= "Joined via a peptide linkage to Phe1"
XX	OS	Synthetic.	
XX	WO9634012-A1.		
XX	PA		
XX	PD	04-FEB-1998; 98US-0073690.	
XX	XX		
XX	PA	(UYPE-) UNIV PENNSYLVANIA.	
XX	PN		
XX	PR	04-FEB-1999; 99WO-US02405.	
XX	XX		
XX	PL	Kieber-Emmons T;	
XX	XX		
XX	DR	WPI; 1999-527317/44.	
XX	XX		
XX	PT	Peptides and recombinant antibody mimics of carbohydrate antigens,	
XX	PT	used for, e.g. treatment of cancer and infection	
XX	XX		
XX	PS	Claim 21; Page 72; 88pp; English.	
XX	XX		
XX	CC	This invention describes a novel method for preparing a peptide or	
XX	CC	recombinant antibody, which mimics an antigenic carbohydrate. The	
XX	CC	peptides and recombinant antibodies prepared to mimic antigenic	
XX	CC	carbohydrates can be used to enhance binding of anti-antigenic	
XX	CC	carbohydrate antibodies to the antigenic carbohydrate, e.g. as vaccine	
XX	CC	adjuvants. The peptides can be used to inhibit binding of a ligand to a	
XX	CC	receptor, which is an antigenic carbohydrate. The methods are used to	
XX	CC	prepare the peptides and antigenic antibodies, which mimic the antigenic	
XX	CC	carbohydrates. Carbohydrate-conjugate vaccines could be used in tumour	
XX	CC	immunity and cancer therapy. The peptides and antibodies can also be	
XX	CC	used as antibacterials. Peptides that mimic carbohydrate antigens can be	
XX	CC	formulated to develop a longer lasting immune response. Other advantages	
XX	CC	of the peptide mimics are: (1) the chemical composition and purity of	
XX	CC	synthesized peptides can be precisely defined; (2) the immunogenicity	
XX	CC	of the peptides can be significantly enhanced by polymerization or	
XX	CC	addition of relatively small carrier molecules that reduce the total	
XX	CC	amount of antigen required for immunization; (3) peptide synthesis may	
XX	CC	be more practical than synthesis of carbohydrate-protein conjugates or	
XX	CC	the production of anti-idiotypes; (4) peptide mimicking sequences can	
XX	CC	be engineered into DNA plasmids for DNA vaccination to further	
XX	CC	manipulate T cell responses. AAY3028-Y3087 represent the carbohydrate	
XX	CC	antigen peptide mimotopes described in the invention.	
XX	SQ	Sequence 5 AA;	
XX	Query Match	75.0%; Score 15; DB 17; Length 5;	
XX	Best Local Similarity	40.0%; Pred. No. 7.7e+05;	
XX	Matches	2; Conservative 0; Mismatches 3;	
XX	Oy	1 FXXXW 5	
XX	Db	1 FSLMW 5	
RESULT 4	RESULT 5		
AAV33038	AAB07280		
ID	AAV33038 standard; peptide; 5 AA.		
XX	AC		
XX	AAV33038;		
XX	DT	17-OCT-2000 (first entry)	
XX	DE	Motif binding to anti-Lewis antigen antibody BR55-2.	
XX	KW	Human; peptido-mimetic; tumour metastasis; E-selectin;	
XX	KW	adhesion molecule; Lewis antigen; anti-adhesion therapy.	
DE	OS	Unidentified.	

XX
PN WO200027420-A1.
XX
PD 18-MAY-2000.
XX
PF 05-NOV-1999; 99WO-US26277.
XX
PR 06-NOV-1998; 98US-0107478.
XX
PA (WISTAR) INST ANATOMY & BIOLOGY.
PA (UYPE) UNIV PENNSYLVANIA.
XX
PI Blaszczyk-Thurin M, Kieber-Emmons T;
XX DR 02-APR-1990; 90JP-0087827.
XX PR 02-APR-1990; 90JP-0087827.
XX PA (SUNR) SUNTORY LTD.
PS Example 5; Page 37; 10pp; English.
XX
CC Tumour metastasis requires detachment of malignant cells from the primary
CC tumour, penetration of blood or lymph vessels and attachment to the
CC endothelium of distant organs, ultimately resulting in the formation of
CC new tumours. The selectin family of adhesion molecules is implicated in
CC this process. E-selectin is a calcium-dependent molecule expressed by
CC activated vascular endothelial E-selectins bind to glycoconjugates
CC carrying a terminal tetrasaccharide Lewis Y antigen, which are found on
CC tumour cell surfaces. One such Lewis antigen is Lewis Y (LeY). The
CC binding of selectin molecules to their ligands is thought to be an
CC important step in metastasis. Therefore, inhibition of
CC E-selectin-dependent carbohydrate-mediated interactions is thought to
CC be a target for anti-cancer therapy. The present sequence is a non
CC planar-X-planar type motif. This motif is thought to bind to anti-LeY
CC antibody BR35-2. BR35-2 is a peptido-mimetics of E-selectins. Peptides
CC that block E-selectin-leY binding and therefore adhesion of tumour cells
CC and leukocytes to endothelial cells inhibit metastasis.
XX
SQ Sequence 5 AA:
Query Match 75.0%; Score 15; DB 21; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 1 FAPGW 5
XX
RESULT 6
AAR26471 AAR26471 standard; peptide; 5 AA.
ID AAR26471;
AC AAR26473;
XX DT 22-OCT-1992 (first entry)
XX DE Serotonin release inhibitor peptide.
XX KW Ganglion; konaganishi; tortoise roll shell; nervous; muscular;
KW system; neurotransmitter; psychotropic; circulatory; drug.
XX OS Tortoise roll shell.
XX PN JP04091096-A.
XX PD 24-MAR-1992.
XX PF 02-APR-1990; 90JP-0087827.
XX PR 02-APR-1990; 90JP-0087827.
XX PA (SUNR) SUNTORY LTD.
XX DR WPI; 1992-14803/18.
XX New glycyl-trypophan and oligopeptide(s) contg. it - esp.
PT alanyl-prolyl deriv., as serotonin release inhibitor for
PT psychotropic and circulatory agent and control of monoamine or
PT peptide neuro-transmitter
XX
PS Claim 1; Page 1; 10pp; Japanese.
XX
CC The peptide (or forms of it truncated from the N-terminus) was prep'd.
CC by extraction from ganglion of konaganishi (tortoise roll shell),
CC with organic solvent, adsorption chromatography and gel filtration.
CC The oligopeptide is a useful reagent in biology or medical science
CC relating to the physiology of the nervous muscular system. It can
CC also be used for controlling monoamine or peptide neurotransmitter
CC relating reactions (e.g. inhibiting serotonin release) and as a
CC psychotropic or circulatory drug.
See also AAR26472-3.

CC See also AAR26471-3.
 XX
 SQ Sequence 5 AA;

RESULT 8
 XX
 Query Match 70.0%; Score 14; DB 13; Length 5;
 Best Local Similarity 40.0%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;
 OY 1 FXXXW 5
 |
 Db 1 FSPGW 5

AC AAR29438
 AC AAR29438 standard; peptide; 5 AA.
 XX
 DE Endothelin antagonist peptide.

XX
 KW Hypertension; myocardial infarction; congestive heart failure;
 KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
 KW acute renal failure; preeclampsia; diabetes; metabolic;
 KW endocrinological; neurological; disorders.
 XX
 OS Synthetic.

XX
 FH Key
 FT Modified-site Location/Qualifiers
 FT 1 /note= "(Ac- or 1-adamantyl acetic acid) - D-Phe"
 PN W09220706-A.
 XX
 PD 26-NOV-1992.
 XX
 PF 24-APR-1992; 92WO-US03408.
 XX
 PR 16-MAY-1991; 91US-0701274.
 PR 18-DEC-1991; 91US-0809746.
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Cody WL, Depue P, Doherty AM, Taylor MD;
 XX
 DR WPI: 1992-415706/50.
 XX
 PT New peptide(s) used as endothelin antagonists - for treating
 PT hypertension, metabolic and endocrine disorders, heart failure,
 PT diabetes, asthma, neurological disorders, etc.
 XX
 PS Claim 5; Page 95; 116pp; English.
 XX
 CC The peptide is an endothelin antagonist useful in controlling
 CC hypertension, myocardial infarction, congestive heart failure,
 CC endotoxic shock, subarachnoid haemorrhage, asthma, arrhythmias,
 CC acute renal failure, preeclampsia, diabetes and metabolic,
 CC endocrinological and neurological disorders. Administration is oral
 CC parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/
 XX day. It may be prepared by conventional peptide synthesis.
 XX
 SO Sequence 5 AA;

RESULT 9
 XX
 Query Match 70.0%; Score 14; DB 13; Length 5;
 Best Local Similarity 40.0%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;
 OY 1 FXXXW 5
 |
 Db 1 FLDIW 5

AC AAR4736
 AC AAR4736 standard; peptide; 5 AA.
 XX
 DE Cyclic peptide which modulates endothelin activity.
 XX
 KW Cyclic; peptide; endothelin; inhibitor; receptor; detection;

KW	isolation; antagonist; hypertension; pulmonary hypertension;
KW	cardiovascular disease; bronchoconstriction; asthma;
KW	inflammatory disease; ophthalmologic shock; anaphylactic shock;
KW	haemorrhagic shock; gastroenteric disease; renal failure;
KW	endotoxin shock; menstrual disorders; obstructive conditions;
KW	erythropoietin-mediated vasoconstriction; wound treatment.
FH	Location/Qualifiers
FT	Misc-difference 1 /note= "Ac-D-Phe"
FT	Misc-difference 1 /note= "D-Tyr bonded to D-Trp at position 5."
FT	Misc-difference 3 /label= D-Ala.
FT	Misc-difference 5 /note= "D-Trp bonded to D-Tyr at position 1."
PA	WO9325580-A.
PA	WO9325580-A.
PT	23-DEC-1993.
XX	17-JUN-1993; 93WO-US05788.
PF	18-JUN-1992; 92US-0900620.
PR	18-JUN-1992; 92US-0900711.
XX	PA (IMMU-) IMMUNOPHARMACEUTICS INC.
PA	PA Balaji VN, Chan MF;
DR	DR WPT; 1994-007458/01.
XX	PT New cyclic peptide(s) which modulate endothelin activity - used for treating endothelin-mediated disorders such as cardiovascular and respiratory diseases
PT	PT New cyclic peptide(s) which modulate endothelin activity - used for treating endothelin-mediated disorders such as cardiovascular and respiratory diseases
XX	PS Claim 2; Page 51; 58pp; English.
CC	The peptide inhibits binding of endothelin-1 (ET) to ERA receptors and/or to ETB receptors. It can be used for detecting, distinguishing and isolating ET receptor subtypes. The peptides also act as ET antagonists and can be used to treat endothelin-mediated disorders such as hypertension, pulmonary hypertension, cardiovascular disease, bronchoconstriction, asthma, inflammatory diseases, ophthalmologic shock, anaesthetic shock, haemorrhagic shock, gastroenteric disease, renal failure, endotoxin shock, menstrual disorders, obstetric conditions, erythropoietin-mediated vasoconstriction and wounds.
SQ	Sequence 5 AA:
CC	Query Match 70.0%; Score 14; DB 15; Length 5; Best Local Similarity 20.0%; Pred. No. 7.7e+05; Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC	Query 1 FXXXW 5 Db 1 FLDIW 5
CC	Sequence 5 AA:
SQ	Query Match 70.0%; Score 14; DB 15; Length 5; Best Local Similarity 40.0%; Pred. No. 7.7e+05; Matches 2; Conservative 2; Mismatches 0; Indels 3; Gaps 0;
CC	Query 1 FXXXW 5 Db 1 FLDIW 5
RESULT 12	AR69260
AC	AR69260 standard; peptide; 5 AA.
XX	ID AR69260
AC	AR69260;
XX	AC
DT	07-MAR-1995 (first entry)
XX	DE Endothelin C-terminal peptide analog, useful as antagonist.
XX	KW Endothelin; ET-1; receptor; antagonist.
OS	OS Synthetic.
OS	SYNTHETIC.
OS	SYNTHETIC.
KEY	Location/Qualifiers
FT	Misc-difference 1 /note= "Ac-D-Phe"
FT	Misc-difference 1 /note= "Ac-D-Phe"
XX	PN WO9414843-A.
XX	PD 07-JUL-1994.
XX	XX 17-DEC-1993; 93WO-US12377.
XX	XX 21-DEC-1992; 92US-095480.
XX	PA (WARN) WARNER LAMBERT CO.
XX	PI Cody WL, Depue P, Doherty AM, He JX, Taylor MD;
XX	PR WPI; 1994-234617/28.
XX	PT New hexapeptide derivs. inhibiting endothelin - for treatment of e.g. renal failure, hypertension, asthma, restenosis, angina, cancer etc.
XX	PT The peptides are useful for treating hypertension, metabolic and endocrine disorders, congestive heart failure, myocardial infarction, endotoxic shock, subarachnoid hemorrhage, arrhythmia, asthma, acute and chronic renal failure, preeclampsia, diabetes, neurological disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel disease, gastric mucosal damage, Raynaud's disease, restenosis, percutaneous transluminal coronary angioplasty, angina and cancer.
XX	CC Novel antagonists of endothelin are claimed which are C-terminal hexapeptides and analogs of ET-1. The first (N-terminal) amino acid of the new peptides has D-configuration. The peptides are claimed generically. The present peptide is a specifically claimed example of the generic compounds.
CC	CC The peptides are useful for treating hypertension, metabolic and endocrine disorders, congestive heart failure, myocardial infarction, endotoxic shock, subarachnoid hemorrhage, arrhythmia, asthma, acute and chronic renal failure, preeclampsia, diabetes, neurological disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel disease, gastric mucosal damage, Raynaud's disease, restenosis, percutaneous transluminal coronary angioplasty, angina and cancer.
XX	CC Sequence 5 AA:
CC	Query Match 70.0%; Score 14; DB 15; Length 5; Best Local Similarity 40.0%; Pred. No. 7.7e+05; Matches 2; Conservative 2; Mismatches 0; Indels 3; Gaps 0;
CC	Query 1 FXXXW 5 Db 1 FLDIW 5
RESULT 11	AR69220
AC	AR69220 standard; peptide; 5 AA.
XX	ID AR69220
AC	AR69220;
XX	AC
DT	06-MAR-1995 (first entry)
XX	DE Endothelin C-terminal peptide analog, useful as antagonist.
XX	KW Endothelin; ET-1; receptor; antagonist.
OS	OS Synthetic.
OS	SYNTHETIC.
KEY	Location/Qualifiers
FT	Misc-difference 1 /note= "Ac-D-Phe"
FT	Misc-difference 1 /note= "Ac-D-Phe"
XX	PN WO9414843-A.
XX	PD 07-JUL-1994.
XX	XX 17-DEC-1993; 93WO-US12377.
XX	XX 21-DEC-1992; 92US-095480.
XX	PR

PA (WARN) WARNER LAMBERT CO.
 XX
 PI Cody WL, Depue P, Doherty AM, He JX, Taylor MD;
 XX DR WPI; 1994-234617/28.
 PT New hexa-peptide derivs. inhibiting endothelin - for treatment of
 PT e.g. renal failure, hypertension, asthma, restenosis, angina,
 XX cancer etc.
 PS Claim 5; Page 120; 146pp; English.
 XX
 CC Novel antagonists of endothelin are claimed which are C-terminal
 CC hexapeptides and analogs of ET-1. The first (N-terminal) amino acid
 CC of the new peptides has D-configuration. The peptides are claimed
 generically. The present peptide is a specifically claimed example
 CC of the generic compounds.
 CC The peptides are useful for treating hypertension, metabolic and
 CC endocrine disorders, congestive heart failure, myocardial infarction,
 CC endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute
 CC and chronic renal failure, preeclampsia, diabetes, neurological
 CC disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel
 CC disease, gastric mucosal damage, Raynaud's disease, restenosis,
 CC percutaneous transluminal coronary angioplasty, angina and cancer.
 XX SQ Sequence 5 AA:
 Query Match 70.0%; Score 14; DB 15; length 5;
 Best Local Similarity 40.0%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 XX Db 1 FDFIW 5
 RESULT 13
 AAR69210
 ID AAR69210 standard; peptide; 5 AA.
 XX
 AC AAR69210;
 XX
 DT 06-MAR-1995 (first entry)
 DE Endothelin C-terminal peptide analog, useful as antagonist.
 XX KW Endothelin; ER-1; receptor; antagonist.
 XX OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "Ac-D-Phe or Ada-D-Phe, where Ada is
 XX 1-adamantyl-acetyl"
 PN WO9414843-A.
 XX
 PD 07-JUL-1994.
 XX
 PF 17-DEC-1993; 93WO-US12377.
 XX
 PR 21-DEC-1992; 920US-0395480.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PT Cody WL, Depue P, Doherty AM, He JX, Taylor MD;
 XX DR WPI; 1994-234617/28.
 XX
 PT New hexa-peptide derivs. inhibiting endothelin - for treatment of
 PT e.g. renal failure, hypertension, asthma, restenosis, angina,
 PT cancer etc.
 XX
 PS Claim 67; Page 32; 138pp; English.

PS Claim 5; Page 118; 146pp; English.
 XX
 ID AAR89837
 ID AAR89837 standard; peptide; 5 AA.
 XX AC AAR89837;
 XX DT 24 JUN 1996 (first entry)
 DE Melanotrophic release inhibiting factor (MIF) modified peptide analogue.
 XX KW MIF; melanotrophic release inhibiting factor; modified; analogue;
 KW hormone; low dosage; L-propyl L-leucyl glycine;
 KW melanocyte stimulating inhibitory factor.
 XX OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "4-F-Phe"
 FT Modified-site 2
 FT /label= OTHER
 FT /note= "Homo-Pro"
 FT Modified-site 5
 FT /label= OTHER
 FT /note= "amidated"
 XX PN WO9530430-A1.
 XX PD 16-NOV-1995.
 XX PP 02-MAY-1995; 95WO-US055660.
 XX PR 04-MAY-1994; 94US-0238089.
 XX PA (INNA) INNAPHARMA INC.
 XX PI Abajian HB, Hlavka JJ, Noble JF;
 XX DR WPI; 1995-403936/51.
 XX
 PT New tri-, tetra-, penta- and poly-peptide cpds. - based on the
 PT tri-peptide hormone melanocyte stimulating inhibitory factor, used
 PT for treating depression
 XX
 PS Claim 67; Page 32; 138pp; English.

CC AAR89786-R89858 are small peptide compounds based on the tripeptide
 CC hormone melanotrophic release inhibiting factor (MIF), also known as
 CC L-propyl L-leucyl glycine and melanocyte stimulating inhibitory
 CC factor. The peptides are used for treating depression and can be
 CC administered so as to achieve a circulating plasma level of 30-90 mg
 CC per average human adult. The peptides show greater anti-depressant
 CC activity than MIF. They can be administered at lower dosage than
 CC known anti-depressants which reduces potential deleterious side
 CC effects.

SQ	Sequence	5 AA:
Qy	1 FXXW 5	Score 14; DB 16; Length 5;
Db	1 FXRGW 5	Best Local Similarity 60.0%; Pred. No. 7.7e+05; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 15

AAR9842

ID AAR9842 standard; peptide; 5 AA.

XX

AC AAR9842;

XX

DT 24-JUN-1996 (first entry)

XX

DE Melanotrophic release inhibiting factor (MIF) modified peptide analogue.

XX

KW MIF; melanotrophic release inhibiting factor; modified; analogue;

KW hormone; low dosage; L-propyl L-leucyl glycine;

KW melanocyte stimulating inhibitory factor.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT /note= "4-F-Phe"

FT Modified-site 2

FT /label= OTHER

FT /note= "Homo-Pro"

FT Modified-site 5

FT /label= OTHER

FT /note= "amidated"

XX

PN WO9530430-A1.

XX

PD 16-NOV-1995.

XX

PF 02-MAY-1995; 95WO-US05560.

XX

PR 04-MAY-1994; 94US-023089.

XX

PA (INNA-) INNAPHARMA INC.

XX

PI Abajian HB, Hlavka JJ, Noble JF;

DR WPI; 1995-403936/51.

PS

XX New tri-, tetra-, penta- and poly-peptide cpds. - based on the
 CC horfnone melanotrophic release inhibiting factor (MIF), also known as
 CC L-propyl L-leucyl glycine and melanocyte stimulating inhibitory
 CC factor. The peptides are used for treating depression and can be
 CC administered so as to achieve a circulating plasma level of 30-90 mg

CC per average human adult. The peptides show greater anti-depressant
 CC activity than MIF. They can be administered at lower dosage than
 CC known anti-depressants which reduces potential deleterious side
 CC effects.

SQ	Sequence	5 AA:
Qy	1 FXXW 5	Score 14; DB 16; Length 5;
Db	1 FXRGW 5	Best Local Similarity 60.0%; Pred. No. 7.7e+05; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Search completed: January 29, 2003, 14:22:04

Job time : 35 secs

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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:22:59 ; Search time 10 seconds
 Sequence: (without alignments)
 10.089 Million cell updates/sec

Title: US-09-403-440A-4

Perfect score: 20

Sequence: 1 FXXXW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 12226 seqs, 20176551 residues

Total number of hits satisfying chosen parameters:

2031

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

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3: /cgpn2_6/ptodata/1/pubpaa/YUS05_NEW_PUB_pep: *

4: /cgpn2_6/ptodata/1/pubpaa/YUS05_NEW_PUBCOMB_pep: *

5: /cgpn2_6/ptodata/1/pubpaa/YUS07_PUBCOMB_pep: *

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10: /cgpn2_6/ptodata/1/pubpaa/YUS09_PUBCOMB_pep: *

11: /cgpn2_6/ptodata/1/pubpaa/YUS10_NEW_PUB_pep: *

12: /cgpn2_6/ptodata/1/pubpaa/YUS10_PUBCOMB_pep: *

13: /cgpn2_6/ptodata/1/pubpaa/YUS60_NEW_PUB_pep: *

14: /cgpn2_6/ptodata/1/pubpaa/YUS60_PUBCOMB_pep: *

15: /cgpn2_6/ptodata/1/pubpaa/YUS60_PUBCOMB_pep: *

16: /cgpn2_6/ptodata/1/pubpaa/YUS60_PUBCOMB_pep: *

17: /cgpn2_6/ptodata/1/pubpaa/YUS60_PUBCOMB_pep: *

18: /cgpn2_6/ptodata/1/pubpaa/YUS60_PUBCOMB_pep: *

19: /cgpn2_6/ptodata/1/pubpaa/YUS60_PUBCOMB_pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1

US-09-214-371-2

; Sequence 2, Application US/09214371B

; Patent NO. US2001018511A1

; GENERAL INFORMATION:

; APPLICANT: Lane, David

; APPLICANT: Bottger, Volker

; APPLICANT: Bottger, Angelica

; APPLICANT: Picklesley, Stephen

; APPLICANT: Chene, Patrick

; APPLICANT: Hochkeppel, Heinz-Kurt

; APPLICANT: Garcia-Echeverria, Carlos

; APPLICANT: Furset, Pascal

; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2

; FILE REFERENCE: 4-20937/A/PCT

; CURRENT APPLICATION NUMBER: US/09-214,371B

; CURRENT FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: PCT/EP97/03549

; PRIOR FILING DATE: 1997-07-04

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 2

; LENGTH: 5

; TYPE: PR1

; ORGANISM: Artificial sequence

; FEATURE: Artificial sequence

; OTHER INFORMATION: Description of Artificial Sequence:peptide

; OTHER INFORMATION: Where Xaa may be any amino acid

; OTHER INFORMATION: Where Xaa may be any amino acid

; OTHER INFORMATION: Where Xaa may be any amino acid

QY	1 FXXXW 5		Db	1 FXXLW 5
Query Match	70.0%	Score 14;	DB 10;	Length 5;
Best Local Similarity	80.0%	Pred. No. 9.9e-04;	Mismatches 0;	Gaps 0;
Matches 4;	Conservative	Indels 0;		

Patent No. US20020061539A1
GENERAL INFORMATION:
APPLICANT: Baxter, John D.
APPLICANT: Dartmont, Beatrice
APPLICANT: Feng, WeiJun
APPLICANT: Fleterick, Robert J.
APPLICANT: Kusner, Peter J.
APPLICANT: Wagner, Richard L.
APPLICANT: West, Brian
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
TITLE OF INVENTION: COACTIVATOR BINDING
FILE REFERENCE: UCAL-253-02US
CURRENT APPLICATION NUMBER: US/09/281,717
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: US 60/079,956
EARLIER FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 3
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (2)-(3)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-281-717-3

Query Match 70.0%; Score 14; DB 10; Length 5;
best Local Similarity 80.0%; Pred. No. 9.9e+04; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXXW 5
Db 1 FXLW 5

RESULT 3
US-08-239-765B-4
; Sequence 4, Application US/08239765B
; patent No. US2002006150A1
GENERAL INFORMATION:
APPLICANT: Savakis, Charalampos
APPLICANT: Franz, Gerald H.
APPLICANT: Loukaris, Athanasios
TITLE OF INVENTION: Eukaryotic Transposable Element
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SBED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/484,409
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 69068.409C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4400
TELEFAX: (206) 632-6031
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-484-409-35

Query Match 55.0%; Score 11; DB 8; Length 5;
best Local Similarity 100.0%; Pred. No. 9.9e+04; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 2 W 2

RESULT 4
US-08-484-409-35
; Sequence 35, Application US/08484409
; patent No. US20020076412A1
GENERAL INFORMATION:
APPLICANT: Steinman, Laurence
APPLICANT: Zanvill, Scott
TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: SBED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/484,409
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 69068.409C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4400
TELEFAX: (206) 632-6031
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-484-409-35

Query Match 55.0%; Score 11; DB 8; Length 5;
best Local Similarity 100.0%; Pred. No. 9.9e+04; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 2 W 2

RESULT 5
US-08-424-550B-228
; Sequence 228, Application US/08424550B
; patent No. US2002011947A1
GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS ;
 APPLICANT: TAMI J. PILOT-MATIAS ;
 APPLICANT: GEORGE J. DAWSON ;
 APPLICANT: GEORGE G. SCHLAUDER ;
 APPLICANT: SURESH M. DESAI ;
 APPLICANT: THOMAS P. LEARY ;
 APPLICANT: ANTHONY SCOTT MUERHOFF ;
 APPLICANT: JAMES C. ERKER ;
 APPLICANT: SHERI L. BUIJK ;
 APPLICANT: ISA K. MUSHAHWAR ;
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/08/424,550B
 FILING DATE:
 CLASSIFICATION: 435435
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMBSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 469:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPeLOGY: linear
 MOLECULE TYPE: protein
 US-08-424-550B-469
 INFORMATION FOR SEQ ID NO: 228:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPeology: linear
 MOLECULE TYPE: protein
 US-08-424-550B-228
 RESULT 6
 Query Match 55.0%; Score 11; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 W 5
 Db 4 W 4
 ; Sequence 14, Application US/09995749A
 ; Patent No. US2002015558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN GEL-SCHUTTEN, GERRITDINA HENDRIKA
 ; APPLICANT: DIJKHUIZEN, LUBBERT
 ; APPLICANT: RAHAOUI, HAKIM
 ; APPLICANT: LEER, ROBERT JAN
 ; TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
 ; FILE REFERENCE: B043388-CIP
 ; CURRENT APPLICATION NUMBER: US/09/995.749A
 ; CURRENT FILING DATE: 2001-11-29
 ; PRIOR APPLICATION NUMBER: 09/604, 957
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: EPO 00201871.1
 ; PRIOR FILING DATE: 2000-05-25
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Neisseria polysaccharaea
 ; US-09-995-749A-14
 Query Match 55.0%; Score 11; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 W 5
 Db 2 W 2
 ; Sequence 14, Application US/09995749A
 ; Patent No. US2002015558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN N. SIMONS
 ; APPLICANT: TAMI J. PILOT-MATIAS
 ; APPLICANT: GEORGE J. DAWSON
 ; APPLICANT: GEORGE G. SCHLAUDER
 ; APPLICANT: SURESH M. DESAI
 ; APPLICANT: THOMAS P. LEARY
 ; APPLICANT: ANTHONY SCOTT MUERHOFF
 ; APPLICANT: JAMES C. ERKER
 ; APPLICANT: SHERI L. BUIJK
 ; APPLICANT: ISA K. MUSHAHWAR
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 RESULT 8

US-09-764-884-2
; Sequence 2, Application US/09764884
; Patent No. US20020161208A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ03
; CURRENT APPLICATION NUMBER: US/09/764,884
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: xaa equals any of the twenty naturally occurring L-amino acids
; Query Match 55.0%; Score 11; DB 9; Length 5;
; Best Local Similarity 100.0%; Pred. No. 9.9e+04; Mismatches 0; Indels 0; Gaps 0;
; Matches 1; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
; QY 5 W 5
; Db 1 W 1

RESULT 9
US-09-895-593-15
; Sequence 15, Application US/09895593
; Patent No. US2002016949A1
; GENERAL INFORMATION:
; APPLICANT: Pandey, Akhilesh
; APPLICANT: Ozaki, Katsutoshi
; APPLICANT: Baumann, Heinz
; APPLICANT: Levin, Steven D.
; APPLICANT: Farr, Andrew G.
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
; Uses Thereof
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,658
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 16
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: description of Artificial Sequence
; OTHER INFORMATION: replacing type I cytokine receptor conserved motif
; OTHER INFORMATION: in murine TSLPR Polypeptide
; Query Match 55.0%; Score 11; DB 9; Length 5;
; Best Local Similarity 100.0%; Pred. No. 9.9e+04; Mismatches 0; Indels 0; Gaps 0;
; Matches 1; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
; QY 5 W 5
; Db 1 W 1

RESULT 11
US-09-423-800-62
; Sequence 62, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIKAI
; APPLICANT: ISHI, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 62
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; Query Match 55.0%; Score 11; DB 9; Length 5;
; Best Local Similarity 100.0%; Pred. No. 9.9e+04; Mismatches 0; Indels 0; Gaps 0;
; Matches 1; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
; QY 5 W 5
; Db 1 W 1

Query Match 55.0%; Score 11; DB 9; Length 5;
; Best Local Similarity 100.0%; Pred. No. 9.9e+04; Length 5;
; Matches 1; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
; QY 5 W 5
; Db 1 W 1

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Db      | ; APPLICANT: Tomlinson, Ian M
3 w 3   ; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8/039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIORITY NUMBER: GB 9722131.1
; PRIORITY FILING DATE: 1997-10-20
; PRIORITY APPLICATION NUMBER: US 60/065,248
; PRIORITY FILING DATE: 1997-11-13
; PRIORITY APPLICATION NUMBER: US 60/066,729
; PRIORITY FILING DATE: 1997-11-21
; PRIORITY APPLICATION NUMBER: PCT/GB98/03135
; PRIORITY FILING DATE: 1998-10-20
; PRIORITY APPLICATION NUMBER: US 09/511,939
; PRIORITY FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 2 ; SEQ ID NO 211
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; US-09-764-857-2

Query Match      55.0%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      5 w 5
Db      1 w 1

RESULT 13 ; US-09-860-670-2
; Sequence 2, Application US/09860670
; Patent No. US20020163137A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA127P1
; CURRENT APPLICATION NUMBER: US/09/860,670
; CURRENT FILING DATE: 2001-05-21
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; US-09-860-670-2

Query Match      55.0%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      5 w 5
Db      1 w 1

RESULT 14 ; US-09-968-561A-217
; Sequence 217, Application US/09968561A
; Patent No. US2002014642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8/039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIORITY NUMBER: GB 9722131.1
; PRIORITY FILING DATE: 1997-10-20
; PRIORITY APPLICATION NUMBER: US 60/065,248
; PRIORITY FILING DATE: 1997-11-13
; PRIORITY APPLICATION NUMBER: US 60/066,729
; PRIORITY FILING DATE: 1997-11-21
; PRIORITY APPLICATION NUMBER: PCT/GB98/03135
; PRIORITY FILING DATE: 1998-10-20
; PRIORITY APPLICATION NUMBER: US 09/511,939
; PRIORITY FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-968-561A-217

Query Match      55.0%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.9e+04; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      5 w 5
Db      1 w 1

RESULT 14 ; US-09-968-561A-211
; Sequence 211, Application US/09968561A
; Patent No. US2002014642A1
; GENERAL INFORMATION:

```

Wed Jan 29 14:47:54 2003

us-09-403-440a-4.slim5.rapb

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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:22:09 ; Search time 131 Seconds
 (without alignments)
 24.608 Million cell updates/sec

Title: US-09-403-440A-4
 Perfect score: 20
 Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
 Gapext 10.0 , Gapext 0.5

Searched: 4569144 seqs, 64473310 residues

Total number of hits satisfying chosen parameters: 42829

Minimum DB seq length: 5
 Maximum DB seq length: 5

Post-processing: Minimum Match 0%,
 Maximum Match 100%
 Listing first 45 summaries

Database :

Pending Patents_AA_Main:*

1: /cgn2_6/prodata/1/paa/PCTUS_COMB_pep: *
 2: /cgn2_6/prodata/1/paa/US096_COMB_pep: *
 3: /cgn2_6/prodata/1/paa/US07_COMB_pep: *
 4: /cgn2_6/prodata/1/paa/US080_COMB_pep: *
 5: /cgn2_6/prodata/1/paa/US081_COMB_pep: *
 6: /cgn2_6/prodata/1/paa/US082_COMB_pep: *
 7: /cgn2_6/prodata/1/paa/US083_COMB_pep: *
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 18: /cgn2_6/prodata/1/paa/US094_COMB_pep: *
 19: /cgn2_6/prodata/1/paa/US095_COMB_pep: *
 20: /cgn2_6/prodata/1/paa/US096_COMB_pep: *
 21: /cgn2_6/prodata/1/paa/US097_COMB_pep: *
 22: /cgn2_6/prodata/1/paa/US098_COMB_pep: *
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 24: /cgn2_6/prodata/1/paa/US100_COMB_pep: *
 25: /cgn2_6/prodata/1/paa/US101_COMB_pep: *
 26: /cgn2_6/prodata/1/paa/US102_COMB_pep: *
 27: /cgn2_6/prodata/1/paa/US60_COMB_pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15	75.0	5 1 PCT-US99-02405-11	Sequence 11, Appl
2	15	75.0	5 1 PCT-US99-26277-114	Sequence 114, Appl
3	15	75.0	5 20 US-09-601-558-11	Sequence 11, Appl
4	15	75.0	5 22 US-09-831-047B-114	Sequence 114, Appl
5	15	75.0	5 22 US-09-831-047C-114	Sequence 11, Appl
6	75.0	5 22 US-09-894-594-11	Sequence 11, Appl	

ALIGNMENTS

RESULT 1
 PCT-US99-02405-11
 ; Sequence 11, Application PCT/US99/02405
 ; GENERAL INFORMATION:
 ; APPLICANT: Trustees of the University of Pennsylvania
 ; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens
 ; FILE REFERENCE: upn344
 ; CURRENT APPLICATION NUMBER: PCT/US99/02405
 ; CURRENT FILING DATE: 1999-02-04
 ; EARLIER APPLICATION NUMBER: 60-0703, 690
 ; EARLIER FILING DATE: 1998-02-04
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 11
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
 ; PCT-US99-02405-11

Query Match Similarity 75.0%; Score 15; DB 1; Length 5;
 Best Local Similarity 40.0%; Pred. No. 4.2e-06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 1 FSLRW 5


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; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: PCT-US99/02405
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/073, 690
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Novel Sequence
; US-09-894-594-11

Query Match 75.0%; Score 15; DB 22; Length 5;
Best Local Similarity 40.0%; Pred. No. 4.2e+06; Mismatches 0; Indels 3; Gaps 0;
Db 1 FXXXX 5
Db 1 FSILW 5

RESULT 7
PCT-US01-20969-3
; Sequence 3 - Application PC/TUS0120969
; GENERAL INFORMATION:
; APPLICANT: GUY, RODNEY
; APPLICANT: BAXTER, JOHN
; APPLICANT: DARMONI, BEATRICE
; APPLICANT: FENG, WEIJUN
; APPLICANT: ROBERT, FLETCHERICK
; APPLICANT: PEETER, KUSHNER
; APPLICANT: RICHARD, WAGNER
; APPLICANT: BRIAN, WEST
; APPLICANT: YAMAMOTO, KEITH
; APPLICANT: GEISTLINGER, TIMOTHY
; APPLICANT: ARNOLD, JAMES
; APPLICANT: KUNTZ, IRWIN
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 9811-016-228
; CURRENT APPLICATION NUMBER: PCT/US01/20969
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/609, 361
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/609, 361
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 60/113, 146
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: US09/281, 717
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: xaa is any amino acid
; PCT-US01-20969-3

Query Match 70.0%; Score 14; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.2e+05; Mismatches 4; Conservatve 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 FXXXW 5
Db 1 FSILW 5

RESULT 8
US-08-981-122-37
; Sequence 37 - Application US/08981122A
; GENERAL INFORMATION:
; APPLICANT: Matanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981, 122A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: JP 7-176904
; EARLIER FILING DATE: 1995-06-21
; EARLIER APPLICATION NUMBER: PCT/JP95/01734
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 37
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: AMIDATION
; OTHER INFORMATION: sequence of peptides synthesized in Examples 11 and 12 from L- OTHER INFORMATION: Fmoc amino acids by solid phase method using an automatic pep
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
; US-08-981-122-37

Query Match 70.0%; Score 14; DB 13; Length 5;
Best Local Similarity 40.0%; Pred. No. 4.2e+06; Mismatches 0; Indels 3; Gaps 0;
Db 1 FXXXX 5
Db 1 FFFRW 5

RESULT 9
US-09-214-371-2
; Sequence 2 - Application US/09214371B
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelika
; APPLICANT: Pickleay, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PC
; CURRENT APPLICATION NUMBER: US/09/214, 371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: Where xaa may be any amino acid
; US-09-214-371-2

Query Match 70.0%; Score 14; DB 16; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.2e+06; Length 5;

```

Matches 4; conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|||
Db 1 FXXLW 5

RESULT 10
US 09-281-717-3
; Sequence 3, Application US/09281717
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Dartmont, Beatrice
; APPLICANT: Feng, WeiJun
; APPLICANT: Fleterick, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
TITLE OF INVENTION: COACTIVATOR BINDING
FILE REFERENCE: UCAL-253-02V2
CURRENT APPLICATION NUMBER: US/09/281,717
CURRENT FILING DATE: 1998-03-30
EARLIER APPLICATION NUMBER: US 60/079,956
EARLIER FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (2) .. (3)
OTHER INFORMATION: Xaa = Any Amino Acid
US 09-281-717-3

Query Match 70.0%; Score 14; DB 16; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.2e+06; Mismatches 0;
Matches 4; Conservative 1; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|||
Db 1 FXXLW 5

RESULT 11
US 09-403-440A-1
; Sequence 1, Application US/09403440A
; GENERAL INFORMATION:
; APPLICANT: Lane, David Philip
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO
; TITLE OF INVENTION: INHIBITING THE INTERACTION OF p53 AND MDM2
FILE REFERENCE: MEWB25_001APC
CURRENT FILING NUMBER: US/09/403,440A
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: PCT/GB98/01144
PRIOR FILING DATE: 1998-04-20
PRIOR APPLICATION NUMBER: GB 9708092.3
PRIOR FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: UNSURE
LOCATION: 2..3..4
OTHER INFORMATION: Xaa = any amino acid
US 09-403-440A-4

Query Match 70.0%; Score 14; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06; Mismatches 0;
Matches 5; Conservative 0; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|||
Db 1 FXXXW 5

RESULT 13
US 09-609-361-3
; Sequence 3, Application US/09609361
; GENERAL INFORMATION:
; APPLICANT: Guy, Rodney
; APPLICANT: Baxter, John
; APPLICANT: Dartmont, Beatrice
; APPLICANT: Feng, WeiJun
; APPLICANT: Robert, Fleterick
; APPLICANT: Peter, Kushner
; APPLICANT: Richard, Wagner
; APPLICANT: Brian, West
; APPLICANT: Yamamoto, Keith
; APPLICANT: Gelstinger, Timothy
; APPLICANT: Arnold, James
; APPLICANT: Kuntz, Irwin
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR ACTIVITY
FILE REFERENCE: 9811-016-999
CURRENT FILING NUMBER: US/09/609,361
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/079,965
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: US 60/113,146
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: US/09/281,717

OTHER INFORMATION: This represents a consensus sequence representing
OTHER INFORMATION: humans and mice.
NAME/KEY: UNSURE
LOCATION: 2..3..4
OTHER INFORMATION: Xaa = any amino acid

PRIOR FILING DATE: 1999-03-30
 NUMBER OF SEQ ID NOS: 83
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 3
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: misc_feature
 NAME/KEY: (2)..(3)
 LOCATION: (2)..(3)
 OTHER INFORMATION: Xaa is any amino acid
 US-09-609-361-3

Query Match 70.0%; Score 14; DB 20; Length 5;
 Best Local Similarity 80.0%; Pred. No. 4.2e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 1 FXXLW 5

RESULT 14

US-09-957-806A-226
 Sequence 226, Application US/0957806A

GENERAL INFORMATION:

APPLICANT: Roggen, Erwin
 APPLICANT: Ernst, Steffen
 APPLICANT: Svendsen, Allan
 APPLICANT: Friis, Esben
 APPLICANT: Osten, Claus

TITLE OF INVENTION: PROTEIN VARIANTS HAVING MODIFIED IMMUNOGENICITY
 FILE REFERENCE: 10021_204-US

CURRENT APPLICATION NUMBER: US/09/957,806A

CURRENT FILING DATE: 2001-09-21

NUMBER OF SEQ ID NOS: 248

SOFTWARE: PatentIn version 3.1

SEQ ID NO 226

LENGTH: 5

TYPE: PRT

ORGANISM: Betula

US-09-957-806A-226

Query Match 70.0%; Score 14; DB 23; Length 5;
 Best Local Similarity 40.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 1 FIKLW 5

RESULT 15
 US-08-064-111B-22

Sequence 22, Application US/08064111B
 GENERAL INFORMATION:

APPLICANT: Kemp, Bruce E.
 APPLICANT: Nicholson, Geoffrey C.
 APPLICANT: Martin, Thomas J.

APPLICANT: Fenton, Anna J.

APPLICANT: Hammonds, R. Glenn

TITLE OF INVENTION: COMPOUNDS AND COMPOSITIONS WHICH INHIBIT
 TITLE OF INVENTION: BONE RESORPTION
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:

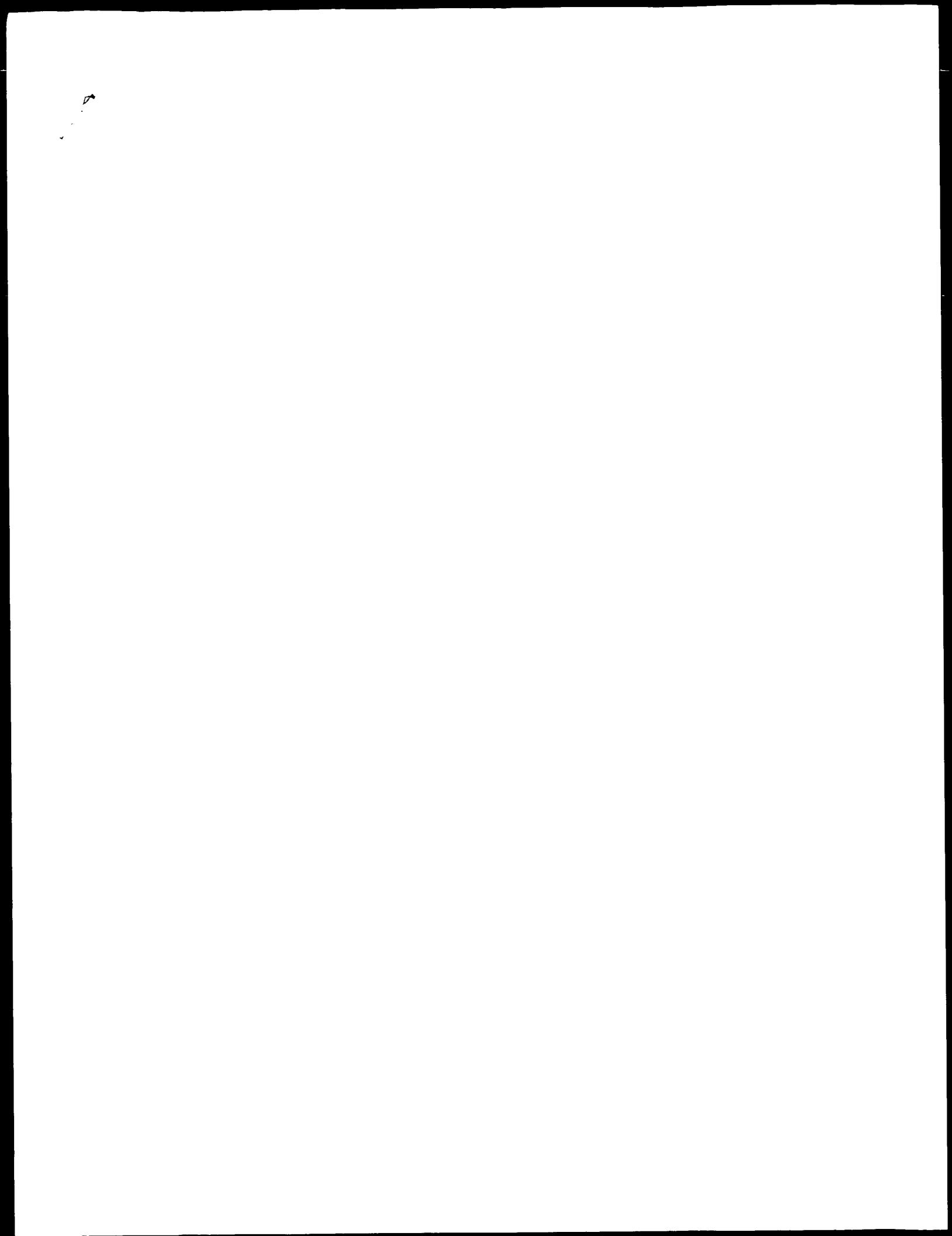
ADDRESSEE: Fleit, Hohbach, Test, Albritton & Herbert,
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/064,111B
 FILING DATE: 12-AUG-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/AU91/00580
 FILING DATE: 13-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU PK9567
 FILING DATE: 19-NOV-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU PK3879
 FILING DATE: 13-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-064-111B-22
 Query Match 65.0%; Score 13; DB 4; Length 5;
 Best Local Similarity 20.0%; Pred. No. 4.2e+06;
 Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 1 YRSAW 5

Search completed: January 29, 2003, 14:25:57
 Job time : 133 secs



ALIGNMENT

Copyright (c) 1993 - 2003 Compugen Ltd.
 GenCore version 5.1.3
 OM protein - protein search, using sw model
 Run on: January 29, 2003, 14:22:24 : Search time 18 Seconds
 (without alignments)
 21.950 Million cell updates/sec
 Title: US-09-403-440A-4
 Perfect score: 20
 Sequence: 1 FXXXW 5
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 396018 seqs, 79020188 residues

PRIOR APPLICATION NUMBER: US 60/414,155
; PRIORITY FILING DATE: 2002-09-27
; PRIORITY APPLICATION NUMBER: US 60/328,624
; PRIORITY FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 65
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide capable of binding to Ang-2
PCT-US02-32657-65

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
QY 5 W 5
Dy 1 W 1

RESULT 3
PCT-US02-33556-34
; Sequence 34, Application PC/TUS0233556
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: PCT/US02/33556
; CURRENT FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-33556-34

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
QY 5 W 5
Dy 1 W 1

RESULT 4
PCT-US02-33556-36
; Sequence 36, Application PC/TUS0233556
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: PCT/US02/33556
; CURRENT FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 36
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 5
PCT-US02-33556-40
; Sequence 40, Application PC/TUS0233556
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: PCT/US02/33556
; CURRENT FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-33556-40

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
QY 5 W 5
Dy 1 W 4

RESULT 6
PCT-US02-33985-2
; Sequence 2, Application PC/TUS0233985
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 16 Human Secreted Proteins
; FILE REFERENCE: PS739PCP
; CURRENT APPLICATION NUMBER: PCT/US02/33985
; CURRENT FILING DATE: 2002-10-24
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 7
PCT-US02-34760-21
; Sequence 21, Application PC/TUS0234760
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hativ, Fortuna
; APPLICANT: Bradley, Michael F.
; TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
; TITLE OF INVENTION: HAVING ANTIANGIOPENIC ACTIVITY
; FILE REFERENCE: 6854.WO.01

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
QY 5 W 5
Dy 1 W 1

Db 2 w 2

RESULT 9
; PCT-US02-34760-47
; Sequence 47, Application PC/TUS0234760
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Haviv, Fortuna
; TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
; FILE REFERENCE: 6854.WO.01
; CURRENT APPLICATION NUMBER: PCT/US02/34760
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 10/263, 811
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 10/000, 540
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/000, 007
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
Db 1 W 1

RESULT 8
PCT-US02-34760-46
; Sequence 46, Application pc/TUS0234760
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Haviv, Fortuna
; APPLICANT: Bradley, Michael F.
; TITLE OF INVENTION: "TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES HAVING ANTIANGIOGENIC ACTIVITY"
; FILE REFERENCE: 6854.WO.01
; CURRENT APPLICATION NUMBER: PCT/US02/34760
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 10/263, 811
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 10/000, 540
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 46

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
Db 2 W 2

RESULT 10
PCT-US02-35606-2
; Sequence 2, Application PC/TUS0235606
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 41 Human Secreted Proteins
; FILE REFERENCE: P5740PCT
; CURRENT APPLICATION NUMBER: PCT/US02/35606
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/331, 046
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

OTHER INFORMATION: Xaa = proethylamide at position 5

NAME/KEY: VARIANT
LOCATION: (5)..(5)

OTHER INFORMATION: Xaa = proethylamide at position 5

NAME/KEY: VARIANT
LOCATION: (2)..(2)

OTHER INFORMATION: Xaa = Nva at position 2

FEATURE:

NAME/KEY: VARIANT
LOCATION: (5)..(5)

OTHER INFORMATION: Xaa = prolylethylamide at position 5

OTHER INFORMATION: Artificial Sequence

TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: VARIANT
LOCATION: (2)..(2)

OTHER INFORMATION: Antiangiogenic Peptide

FEATURE:

NAME/KEY: VARIANT
LOCATION: (5)..(5)

OTHER INFORMATION: Xaa = proethylamide at position 5

OTHER INFORMATION: Xaa = proethylamide at position 5

NAME/KEY: VARIANT
LOCATION: (5)..(5)

OTHER INFORMATION: Xaa = proethylamide at position 5

OTHER INFORMATION: Xaa = proethylamide at position 5

NAME/KEY: Site
LOCATION: (3)

OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

PCT-US02-34760-46

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

PCT-US02-35606-2

```

DE      1 W 1

RESULT 11
PCT-US02/16525A-26
; Sequence 25, Application PC/TUSS0216525A
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF56PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16525A
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293, 212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 5
; SEQ ID NO 26
; LENGTH: 5
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US02/16525A-26

Query Match          55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 W 5
|       |
Db      1 W 1

RESULT 12
PCT-US02/24469-21
; Sequence 21, Application PC/TUSS0224469
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: Biological Assay Detection Method
; FILE REFERENCE: PCT 2000Y
; CURRENT APPLICATION NUMBER: PCT/US02/24469
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/310, 599
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: thioesterase motif
PCT-US02/24310-166

Query Match          55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 W 5
|       |
Db      2 W 2

RESULT 13
PCT-US02/24310-166
; Sequence 166, Application PC/TUSS0224310
; GENERAL INFORMATION:
; APPLICANT: CUBIST PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOXYCIN
; FILE REFERENCE: CUB-12 PCT CIP
; CURRENT APPLICATION NUMBER: PCT/US02/24310
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US01/32354
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/310, 385
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 60/379, 866
; PRIOR FILING DATE: 2002-03-10
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 166
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: thioesterase motif
PCT-US02/24310-166

Query Match          55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 W 5
|       |
Db      2 W 2

RESULT 14
PCT-US02/24469A-21
; Sequence 21, Application PC/TUSS0224469A
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: Biological Assay Detection Method
; FILE REFERENCE: PCT 2000Y
; CURRENT APPLICATION NUMBER: PCT/US02/24469A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/310, 599
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa is a variable which may be
; OTHER INFORMATION: A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, V
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
; PCT-US02/24469-21

Query Match          55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 W 5
|       |
Db      3 W 3

```

Db 3 W 3

RESULT 15

PCT-US02-39109-15

; Sequence 15, Application PC/TUS0239109

GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America, as represented by the

; APPLICANT: Secretary, Department of Health and Human Services

; APPLICANT: Ruscetti, Francis W.

; TITLE OF INVENTION: PEPTIDE T STIMULATES CTL RESPONSES

; FILE REFERENCE: 14014 0404PI

; CURRENT APPLICATION NUMBER: PCT/US02/39109

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: 60/338,971

; PRIOR FILING DATE: 2001-12-07

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence;/note =

; OTHER INFORMATION: Synthetic Construct

; PCT-US02-39109-15

Query Match 55.0%; Score 11; DB 1; Length 5;

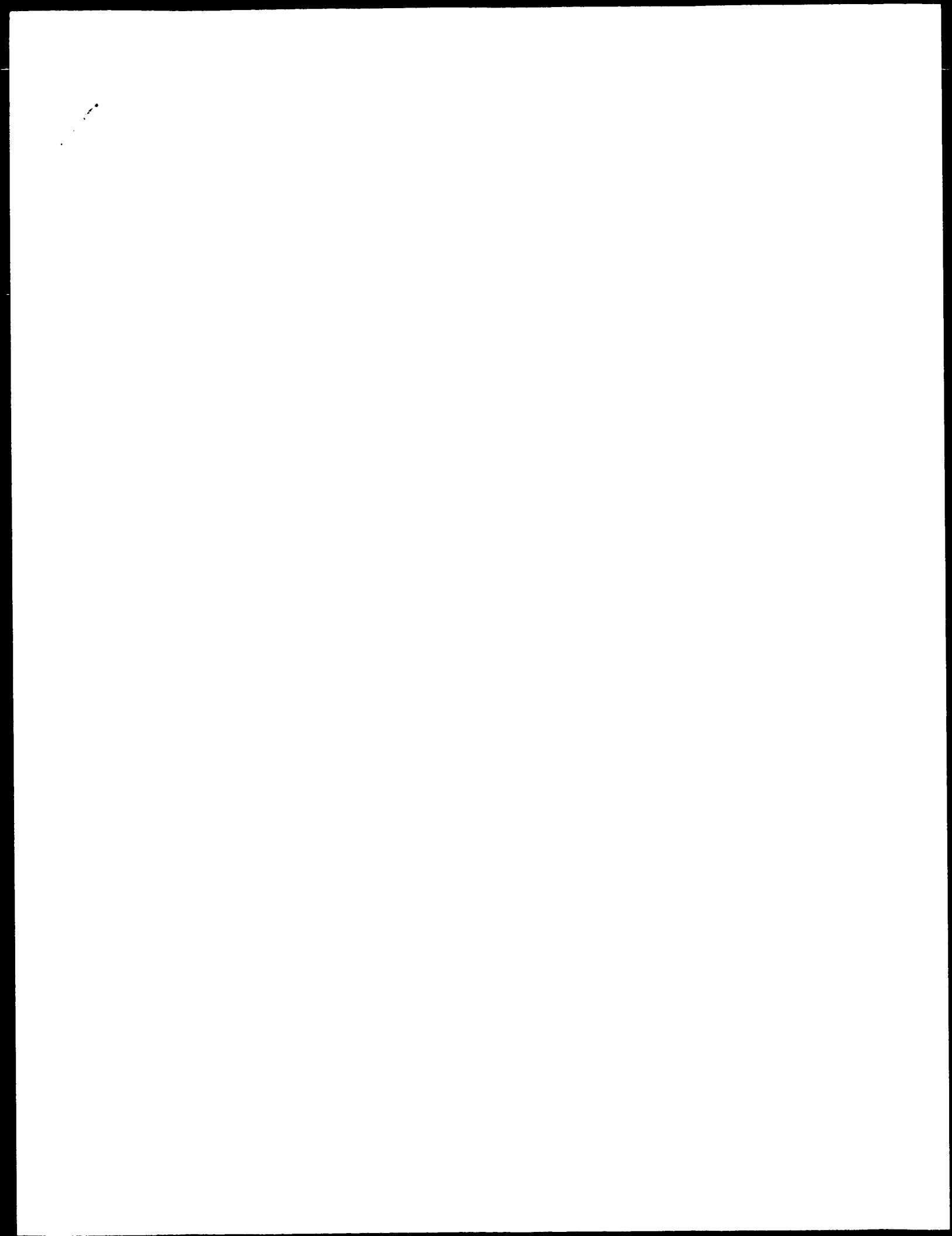
Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5

Db 3 W 3

Search completed: January 29, 2003, 14:26:20
Job time : 18 secs



Run on: January 29, 2003, 14:21:29 ; Search time 14 seconds
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OM protein - protein search, using sw model

Title: Perfect score: US-09-403-440A₁-4

Sequence: 1 FXXXW 5

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 262374 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 10533

Minimum DB seq length: 5
 Maximum DB seq length: 5

Post-processing: Minimum Match 0%, Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A, COMB pep: *
 2: /cgn2_6/ptodata/1/iaa/5B, COMB pep: *
 3: /cgn2_6/ptodata/1/iaa/6A, COMB pep: *
 4: /cgn2_6/ptodata/1/iaa/6B, COMB pep: *
 5: /cgn2_6/ptodata/1/iaa/pctrus, COMB pep: *
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	14	70.0	5	1 US-08-424-957-4 Sequence 4, Appli
2	14	70.0	5	1 US-08-424-957-4 Sequence 5, Appli
3	14	70.0	5	1 US-08-424-957-5 Sequence 37, Appli
4	14	70.0	5	1 US-08-981-122-37 Sequence 4, Appli
5	14	70.0	5	1 US-09-035-686-4 Sequence 5, Appli
6	14	70.0	5	1 US-09-035-686-5 Sequence 3, Appli
7	13	65.0	5	1 US-09-099-2053-3 Sequence 22, Appli
8	13	65.0	5	1 US-08-064-111C-22 Sequence 83, Appli
9	13	65.0	5	1 US-07-789-884-83 Sequence 83, Appli
10	13	65.0	5	1 US-08-475-263-83 Sequence 83, Appli
11	13	65.0	5	1 US-08-485-886-83 Sequence 83, Appli
12	13	65.0	5	2 US-08-477-362-83 Sequence 83, Appli
13	13	65.0	5	3 US-08-473-489A-83 Sequence 83, Appli
14	13	65.0	5	3 US-08-485-695-83 Sequence 83, Appli
15	13	65.0	5	3 US-08-981-122-2 Sequence 83, Appli
16	13	65.0	5	4 US-08-018-760-83 Sequence 83, Appli
17	11	55.0	5	1 US-07-657-769B-15 Sequence 15, Appli
18	11	55.0	5	1 US-07-657-769B-16 Sequence 16, Appli
19	11	55.0	5	1 US-07-657-769B-17 Sequence 17, Appli
20	11	55.0	5	1 US-07-657-769B-18 Sequence 18, Appli
21	11	55.0	5	1 US-07-657-769B-19 Sequence 19, Appli
22	11	55.0	5	1 US-07-657-769B-20 Sequence 20, Appli
23	11	55.0	5	1 US-07-657-769B-21 Sequence 21, Appli
24	11	55.0	5	1 US-07-657-769B-22 Sequence 22, Appli
25	11	55.0	5	1 US-07-657-769B-36 Sequence 36, Appli
26	11	55.0	5	1 US-07-657-769B-37 Sequence 37, Appli
27	11	55.0	5	1 US-07-657-769B-38 Sequence 38, Appli

ALIGNMENTS

RESULT 1
 US-08-424-957-4

SEQUENCE: FXXXW 5

PATENT NO. 5770377

GENERAL INFORMATION:

APPLICANT: PICKSLEY, Steven M.

APPLICANT: Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDM2 and P53 Protein and Therapeutic Application Thereof

NUMBER OF ISQUENCES: 50

CORRESPONDENCE ADDRESS:

ADRESSEEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/424, 957

FILING DATE: 19-APR-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/277, 660

FILING DATE: 20-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-61228/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

US-08-424-957-4

Query Match Score: 70.0%; Length: 5;

Best Local Similarity: 80.0%; Pred. No. 1 9e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db
1 FXXXW 5
|||||

; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: AMIDATION

RESULT 2
US-08-424-957-5
; Sequence 5, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Pickslay, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Flehr, Holbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424, 957
; FILING DATE: 19-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24, 190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277-99
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-5

Query Match 70.0%; Score 14; DB 3; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 1 FPPRW 5
|||||

RESULT 4
US-09-035-686-4
; Sequence 4, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickslay, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Flehr, Holbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035, 686
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24, 190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277-99
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-4

Query Match 70.0%; Score 14; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 1 FXELW 5
|||||
RESULT 3
US-08-981-122-37
; Sequence 37, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Akitomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981, 122B
; CURRENT FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; PRIOR FILING DATE: 1996-06-21

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 5
 US-09-035-686-5
 QY 1 FXXXW 5
 |||
 Db 1 FXLW 5

GENERAL INFORMATION:
 APPLICANT: Pickley, Steven M.
 APPLICANT: Lane, David P.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/035, 686
 FILING DATE: CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/424, 957
 FILING DATE: 19-APR-1995
 APPLICATION NUMBER: US 08/277, 660
 FILING DATE: 20-JUL-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-61228/WHD

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEX: (415) 3398-3249
 TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 SPANNEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 FEATURE:
 OTHER INFORMATION: "Xaa" in position 3 stands for either Glu or Asp.

US-09-035-686-5

Query Match 70.0%; Score 14; DB 4; Length 5;
 Best Local Similarity 60.0%; Pred. No. 1.9e+05; 2; Indels 0; Mismatches 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXW 5
 |||
 Db 1 FXLW 5

RESULT 6
 US-09-099-053-3
 Sequence 3, Application US/09099053
 Patient No. 6388063

GENERAL INFORMATION:
 APPLICANT: Greg Plowman
 APPLICANT: Susan Onrust
 APPLICANT: David Markby
 APPLICANT: Sara Courtenage

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

RESULT 7
 US-08-064-111C-22
 Sequence 22, Application US/0806411C
 Patient No. 5688760

GENERAL INFORMATION:
 APPLICANT: Kemp, Bruce E.
 APPLICANT: Nicolson, Geoffrey C.
 APPLICANT: Martin, Thomas J.
 APPLICANT: Renton, Anna J.
 APPLICANT: Hammoud, R. Glenn

TITLE OF INVENTION: COMPOUNDS AND COMPOSITIONS WHICH INHIBIT BONE RESORPTION
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

RESULT 10
US-08-485-886-83
Sequence 83, Application US/08485886
Patent No. 5,798,48
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08477, 362
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/789, 184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29, 959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
TELEX: 34-0154 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLogy: linear
US-08-477-362-83

RESULT 11
US-08-477-362-83
Sequence 83, Application US/08477134
Patent No. 5,564,48
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08477, 134
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/789, 184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29, 959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154 494-0792
INFORMATION FOR SEQ ID NO: 83:

SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-477-134-83

Query Match	65.0%	Score 13;	DB 2;	Length 5;
Best Local Similarity	40.0%	Pred. No.	1.9e+05;	
Matches	2;	Mismatches	3;	Indels 0;
Qy	1 FXXXW 5			Gaps 0;
Db	1 FEPFW 5			

RESULT 13
 US-08-473-482A-83
 Sequence 83; Application US/08473482A
 Patent No. 6024936
 GENERAL INFORMATION:
 APPLICANT: COUGHLIN, SHAUN R.
 APPLICANT: SCARBOROUGH, ROBERT M.
 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES: 223
 NUMBER OF SEQUENCES: RELATED PHARMACEUTICALS
 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES: 223
 ADDRESSSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 ZIP: 94304-1108
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,695
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/7789, 184
 FILING DATE: 07-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22000-20502.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 34-0154
 INFORMATION FOR SEQ ID NO: 83:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-485-695-83

RESULT 14
 US-08-485-695-83
 Sequence 83; Application US/08485695
 Patent No. 6024936
 GENERAL INFORMATION:
 APPLICANT: Hatanoaka, Yoshihiro
 APPLICANT: Arizumi, Masaharu
 TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/08/981,122B
 CURRENT FILING DATE: 1991-12-18
 PRIOR APPLICATION NUMBER: JP 7-176904
 PRIOR FILING DATE: 1995-06-21
 PRIOR APPLICATION NUMBER: PCT/JP96/01734
 PRIOR FILING DATE: 1996-06-21
 NUMBER OF SEQ ID NOS: 90
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:

RESULT 14
 US-08-485-695-83
 Sequence 83; Application US/08485695

; OTHER INFORMATION: Sequence of a peptide synthesized in Example 1 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multipeptide
; OTHER INFORMATION: synthesizing system (RAMPs)
US-08-981-122-2

Query Match 65.0%; Score 13; DB 3; Length 5;
Best Local Similarity 40.0%; Pred. No. 1 9e+05; Mismatches 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; QY 1 FXXW 5
Db 1 FRWW 5

Search completed: January 29, 2003, 14:23:38
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